Chromatin dynamics during interphase and cell division

Pecinka, Ales; Chevalier, Christian; Colas, Isabelle; Kalantidis, Kriton; Varotto, Serena; Krugman, Tamar

Published in:
Journal of Experimental Botany

DOI:
10.1093/jxb/erz457

Publication date:
2019

Document Version
Peer reviewed version

Chromatin dynamics during interphase and cell division: similarities and differences between model and crop plants

Ales Pecinka[1,*], Christian Chevalier[2], Isabelle Colas[3], Kriton Kalantidis[4], Serena Varotto[5], Tamar Krugman[6], Christos Michaelidis[7], María-Pilar Vallés[8], Aitor Muñoz[9] and Mónica Pradillo[10]

[1] The Czech Academy of Sciences, Institute of Experimental Botany; Centre of the Region Haná for Agricultural and Biotechnological Research, Šlechtitelů, Olomouc, Czech Republic
[2] UMR1332 BFP, INRA, University of Bordeaux, Villenave d'Ornon Cedex, France
[3] James Hutton Institute, Cell and Molecular Science, Pr Waugh's lab, Errol Road, Invergowrie, Dundee, Scotland, United Kingdom
[4] Department of Biology, University of Crete, and Institute of Molecular Biology Biotechnology, FoRTH, Heraklion, Greece
[5] Department of Agronomy Animal Food Natural Resources and Environment (DAFNAE) University of Padova, Agripolis viale dell'Università, Legnaro (PD), Italy
[6] Institute of Evolution, University of Haifa, Haifa, Israel
[7] The Czech Academy of Sciences, Institute of Experimental Botany, Rozvojová 263, Praha 6 – Lysolaje, Czech Republic
[8] Department of Genetics and Plant Breeding, Estación Experimental Aula Dei (EEAD), Spanish National Research Council (CSIC), Zaragoza, Spain
[9] Department of Plant Molecular Genetics, National Center of Biotechnology/Superior Council of Scientific Research, Autónoma University of Madrid, Madrid, Spain.
[10] Department of Genetics, Physiology and Microbiology, Faculty of Biology, Complutense University of Madrid, Madrid, Spain

* Correspondence: pecinka@ueb.cas.cz

Abstract

Genetic information in the cell nucleus controls organismal development, responses to the environment and finally ensures own transmission to the next generations. To achieve so many different tasks, the genetic information is associated with structural and regulatory proteins, which orchestrate nuclear functions in time and space. Furthermore, plant life strategies require chromatin plasticity to allow a rapid adaptation to abiotic and biotic stresses. Here, we summarize current knowledge on the organisation of plant chromatin and dynamics of chromosomes during interphase and mitotic and meiotic cell divisions for model and crop plants differing as to the genome size, ploidy and amount of genomic resources available. The existing data indicate that chromatin changes accompany most (if not all) cellular processes and that there are both shared and unique themes in the chromatin structure and global chromosome dynamics among species. Ongoing efforts to understand the molecular mechanisms involved in chromatin organisation and remodeling have, together with the latest genome editing tools, potential to unlock crop genomes for innovative breeding strategies and improvements of various traits.

Keywords: Chromatin, epigenetics, chromosome, mitosis, meiosis, plant development, plant breeding, crops, Arabidopsis.

Introduction

Most eukaryotic DNA, the carrier of genetic information, is stored in cell nuclei as linear supermolecules - the chromosomes. Complexes of nuclear DNA with the associated proteins constitute chromatin, which is required for proper DNA packaging, regulation of gene expression and chromosome organisation. The basic units of chromatin are the nucleosomes, which consist of approximately 146 bp of DNA wrapped around a histone octamer having two copies of each of the H2A, H2B, H3 and H4 (reviewed in e.g. McGinty and Tan, 2015).

Replacing the canonical histones with non-canonical ones leads to different chromatin functions (Koyama and Kurumizaka, 2018). Data from the model species *Arabidopsis thaliana* (Arabidopsis) suggest functional diversification of histone H1, H2A and H3 proteins. Histones H1.1 and H1.2 represent the canonical forms, but H1.3 is a stress inducible variant (Rutowicz *et al.*, 2015). The H2A.Z containing nucleosomes occurs in the transcription start and termination sites of ubiquitously transcribed genes and cover large parts of stress and developmentally regulated genes (Coleman-Derr and Zilberman, 2012). H2A.Z also marks other functional domains, e.g. potential sites of meiotic recombination (Zilberman *et al.*, 2008; Choi *et al.*, 2013; Yelagandula *et al.*, 2014). H2A.X is an evolutionary conserved variant scattered throughout the genome and upon phosphorylation of the serine 139 (γ-H2A.X) labels the sites of DNA damage repair (Friesner *et al.*, 2005; Lorković *et al.*, 2017). The recently discovered plant-specific variant H2A.W occurs in repetitive DNA regions, where it represses transposons and marks the sites of DNA damage repair (Yelagandula *et al.*, 2014; Lorković *et al.*, 2017). The H3 proteins include H3.1, H3.3 and CenH3 (CENP-A), representing the transcriptionally active, inactive and the kinetochore binding regions, respectively (Lermontova *et al.*, 2011; Stroud *et al.*, 2012; Wollmann *et al.*, 2012; Maheshwari *et al.*, 2015). CenH3 receives great attention owing to the fact that its mutations lead to production of haploids, a trait that could be used in the process of double haploid production (Ravi and Chan, 2010; Sanei *et al.*, 2011; Yuan *et al.*, 2014; Karimi-Ashtiyani *et al.*, 2015).

Unstructured histone N-termini (tails) are the rich substrate for post-translational modifications (PTMs) by methylation, acetylation and phosphorylation among others. Acetylation is associated with active chromatin, while methylation can have both permissive and repressive functions depending on the residue and the number of methyl groups in plants.

The most common plant genome DNA modification is cytosine methylation (5-methyl-2'deoxy-cytosine or DNA methylation), where CG, CHG and CHH (H = A, T or C) represent the three functional DNA methylation contexts (Law and Jacobsen, 2010). DNA methylation can be established *de novo* at any cytosine by the RNA-directed DNA methylation (RdDM) pathway guided to the target sequences by small interfering RNAs with the perfect sequence homology (reviewed in e. g. Matzke and Mosher, 2014). Once established, DNA methylation is maintained by the activity of replication-coupled DNA methyltransferases specialized for each cytosine context, and by the corrective activity of RdDM (Du *et al.*, 2012; Zemach *et al.*, 2013; Baubec *et al.*, 2014). So far little is known about the significance and the functions of adenine methylation in plants (Vanyushin *et al.*, 1988; Fu *et al.*, 2015).

Nucleosomal DNA arrays are folded at multiple levels into higher order structures and eventually into the chromosomes (reviewed in e.g. Dixon et al., 2016). Microscopic observations of variable chromatin staining intensity led to the early description of the darker chromosome stain called heterochromatin and the lighter chromosome stain called euchromatin (Heitz, 1928). Molecular experiments revealed that heterochromatin is normally repeat-rich/gene-poor, densely packed, and transcriptionally silent, while euchromatin is open, repeat-poor/gene-rich and transcriptionally active (Roudier *et al.*, 2011; Sequeira-Mendes *et al.*, 2014). Organisation and dynamics of the large chromatin domains and their functional significance in plants seems to be strongly influenced by the nuclear genome size and amount of repetitive DNA, but it is still not well understood. The small genome of Arabidopsis is organised as mostly randomly positioned chromosome territories with nuclear envelope (NE)-associated heterochromatic chromocentres (CCs) and nucleolus associated nucleolar organizer regions (NORs) (Fransz *et al.*, 2002; Pecinka *et al.*, 2004). In contrast, large genomes of e.g. cereals show Rabl-organisation with centromeres and telomeres clustered at the opposite nuclei poles. These patterns have recently been explored in detail by the chromatin conformation capture techniques (reviewed in Doğan and Liu, 2018). Currently, it remains unknown how representative such organisations are for different tissues, under changing environmental conditions and for species with intermediate DNA content. In addition, Hi-C experiments suggest that a combination of different factors, such as genomic composition, epigenetic modification, and transcriptional activity are involved in shaping global and local chromatin packing in Arabidopsis and rice (Grob *et al.*, 2014; Dong *et al.*, 2018). Hi-C applications to other crops will improve our knowledge on the role of chromosomes packing in the nucleus in modifying gene expression under stress conditions.

Chromatin organisation in somatic cell nuclei under ambient and stress conditions

Plants rapidly change gene expression during stress, to make a rational use of the existing resources and to minimize damage. Chromatin changes have been found practically after all types of applied abiotic and biotic stresses, and there is growing evidence that some epigenetic changes play important role in the fine tuning of stress responses (Kim *et al.*, 2010; Ding and Wang, 2015) (Fig. 1).

Nuclei of germinating Arabidopsis seeds appear mostly euchromatic, and heterochromatin is established only in response to the light stimulus (Mathieu *et al.*, 2003). Light-induced heterochromatin re-organisation leads to transcriptional reprogramming and activation of photosynthesis during germination (Bourbousse *et al.*, 2015). Light quality-induced phytochrome signaling may also cause repositioning of specific chromatin regions, e.g. chlorophyll A/B binding (CAB) locus in Arabidopsis, and thus influence gene expression (Feng *et al.*, 2014). Composition and intensity of solar radiation varies strongly depending on the season, geographical location or surrounding vegetation.

Ultraviolet A and B (UV-A/B, 280-400 nm) is the most energetic component of solar radiation, which damages membranes, proteins and DNA, and its intensity increases with

altitude and proximity to equator. Plants probably adapt to UV radiation as indicated by the constitutive expression of chromatin-remodeling factors and reduced sensitivity to UV damage, as was found in maize landraces at the tropical high altitude (Casati *et al.*, 2006, 2008). Interestingly, methyl cytosines have higher propensity to be involved in UV-induced pyrimidine dimers than normal cytosines, and their less efficient repair in heterochromatin leads to conversions into thymines (Willing *et al.*, 2016). Hence, UV radiation has a profound effect on both epigenome and genome stability.

Temperature fluctuations are common and involve rapid adjustment of cellular metabolism, growth and differentiation (Kotak *et al.*, 2007). Heat stress reduces chromatin compaction and coordinated organ specific transcriptional response via changes in nucleosome and H2A.Z occupancy (Kumar and Wigge, 2010; Pecinka *et al.*, 2010; Boden *et al.*, 2013; Lämke and Bäurle, 2017). Severe heat stress modulates chromatin structure, by increasing histone acetylation and decreasing H3K9me2 and eventually induces programmed cell death (Wang *et al.*, 2015*b*). Surprisingly, cold stress also leads to general chromatin de-condensation, as suggested by Hi-C analysis in rice, but specific regions may be subject to chromatin condensation and gene silencing (Liu *et al.*, 2017). Taken together, the data suggest that in a range of optimal temperatures, which are species-specific, chromatin is normally condensed, and de-condenses at suboptimal conditions. However, this hypothesis needs to be tested on a broader range of species and temperatures.

Vernalization is well-known example of cold induced chromatin change, i.e. acquisition of competence to flower only in response to a period of cold. In Arabidopsis, vernalization occurs via H3K27 tri-methylation and silencing of MADS box transcription repressor *FLOWERING LOCUS C* (*FLC*) (Rosa and Shaw, 2013; Whittaker and Dean, 2017). However, vernalization evolved multiple times in plants and its mechanism differs between species (Reeves *et al.*, 2012; Périlleux *et al.*, 2013; Ruelens *et al.*, 2013; Porto *et al.*, 2015). *VERNALIZATION 1* (*VRN1*) is the major vernalization gene in cereals, which loses H3K27me3 and gains H3K4me3 during cold period (Oliver *et al.*, 2009; Diallo *et al.*, 2012). Temperature changes also lead to selective and transient activation of repetitive sequences (Steward *et al.*, 2002; Pecinka *et al.*, 2010; Tittel-Elmer *et al.*, 2010; Ito *et al.*, 2011). Recent studies suggested that this is due to the presence of the canonical cis-regulatory elements in the LTRs of specific stress-responsive transposon families (Cavrak *et al.*, 2014; Pietzenuk *et al.*, 2016). This could represent an evolutionary mechanism of dispersal for cis-regulatory elements in the genome and foundation of novel gene expression patterns (Ito *et al.*, 2011).

Reduced water availability negatively influences yield and resistance to other stresses. Effect of water stress on plant chromatin is not well understood, but data suggest that the responses are species-specific. Drought caused DNA methylation changes in the shoot apical meristems (SAM) of hybrid poplars (Gourcilleau *et al.*, 2010), and there were additional changes in DNA methylation and expression of phytohormone metabolism genes after re-watering (Gourcilleau *et al.*, 2010). In tomato, drought induced DNA methylation changes in

ABSCISIC ACID STRESS AND RIPENING 1 and *2* (*ASR1* and *ASR2*) genes (González *et al.*, 2011, 2013) and thus probably modified the ripening process.

In contrast, no consistent water stress-induced DNA methylation changes were observed in Arabidopsis and maize (Eichten and Springer, 2015; Ganguly *et al.*, 2017). Instead, H3K4me3 may represent a drought stress "memory" mark, which influences the transcriptional response during recurring stress in Arabidopsis (Ding *et al.*, 2012). The topic of chromatin mediated "epigenetic memory" has been recently reviewed in several papers (for example in Jablonka and Raz, 2009; Avramova, 2015; Lämke and Bäurle, 2017), and therefore we do not review it here.

Attacks of crops by pathogens may have severe consequences on plant vitality and yield, and can even cause lethality. Biotic stress defense mechanisms are fast evolving to match the evolutionary innovations on the pathogen side, which leads to a constant race between the host and the pathogen. Following infection by biotrophic or necrotrophic pathogens, plants typically reprogram gene expression from growth to defense (Moore *et al.*, 2011), which involves activation of the salicylic acid (SA) and the jasmonic acid/ethylene (JA/ET) pathways, respectively (reviewed in e.g. Glazebrook, 2005; Vlot et al., 2009). Some pathogens developed strategies to directly affect chromatin modifiers. For example, the necrotrophic fungus *Alternaria brassicola* produces a toxin that inhibits Histone deacetylase (HDA) activity during infection (Matsumoto *et al.*, 1992; Kwon *et al.*, 2003). In line with this, knock-down of Arabidopsis HDA19 led to increased susceptibility to *A. brassicola*, while its overexpression activated JA/ET-regulated genes and triggered pathogen resistance (Zhou *et al.*, 2005). HDA19 represses SA biosynthesis and defense responses in Arabidopsis by suppressing transcription of *PATHOGENESIS RELATED* (*PR*) *PR1* and *PR5* genes (Tian *et al.*, 2005), indicating its negative role in SA-mediated defense responses (Choi *et al.*, 2012). Upon infection by Pst DC3000, *SIRTUIN2* (*SRT2*), another HDA involved in immune responses, is down-regulated, leading to higher SA production and expression of downstream defense genes (Wang *et al.*, 2010). In contrast, some HDAs regulate innate immunity positively (Latrasse *et al.*, 2017*a*). Although it is clear that histone acetylation (and de-acetylation) plays an important role in the regulation of defense-related genes, it is still not clear how HAT and HDAs are targeted to the target loci to allow genome-wide changes in gene expression (Ramirez-Prado *et al.*, 2018).

The effects of viruses on plant chromatin remain only poorly understood. In a pioneer study, Arabidopsis mutants deficient in DNA methylation and RdDM were found to be susceptible to geminiviruses (Raja *et al.*, 2008). The genimivirus genome consists of two single stranded DNA molecules, which replicate using the host's replication machinery. The replicated virus dsDNAs are packed with nucleosomes and form tiny chromosome-like structures. The hosts' defense responses involve suppression of gene expression by methylating the viral genome. Involvement of RNA PolII and RDR6 (Jackel *et al.*, 2016),

indicates that the silencing is triggered by the non-canonical RdDM (reviewed in e.g. Matzke and Mosher, 2014).

In summary, this chapter shows that responses of chromatin to various stresses are diverse and in some cases highly adaptive. In many cases, we have only basic description of the stress-induced chromatin changes, and we still miss information on the persistence of these changes after recovery from the stress and about their heritability through mitosis and meiosis. Therefore, we expect that many future studies will focus on the identification of underlying mechanisms. In addition, it is expected that more groups of chromatin modifiers such as histone (de)methyltransferases and (de)ubiquitinylases will be firmly connected with stress-induced chromatin responses (Dhawan *et al.*, 2009; Wang *et al.*, 2015*a*; Dutta *et al.*, 2017). Understanding the involvement of chromatin in adjusting plant adaptation to diverse environmental challenges is of interest to a broad audience of plant scientists, considering that stresses are generally predicted to become exacerbated due to climate change and that they can strongly affect crop yields.

Chromatin organisation during mitotic and meiotic cell divisions

Chromatin undergoes drastic changes affecting its degree of compaction during the cell cycle. At the onset of cell divisions, the nuclear envelope (NE) disassembles allowing the access of cytoplasmic proteins to the nucleoplasm, including proteins which contribute to further chromatin condensation and spindle formation. Chromatin condensation is critical for the individualisation of chromosomes in order to guarantee proper distribution of genetic information between daughter cells. After segregation, chromatin is decondensed to restore its interphase state. To achieve this process, specific PTMs in histones occur, including the marker of condensed chromatin histone H3S10p (p = phosphorylation) and mitosis-specific PTMs such as histone H3T3p and H3T11p (Houben *et al.*, 2002; Zhang *et al.*, 2005). In maize, histone H3S28p and H3S50p delineate the pericentromeric and centromere regions during chromosome segregation, respectively (Zhang *et al.*, 2005). In the same species, changes in the level of histone H3S10p regulate sister chromatid cohesion (Kaszas and Cande, 2000), and an increase of H3 phosphorylation is linked to reduced acetylation levels at lysine 9 residues in histones H3 (Edmondson *et al.*, 2002). In barley, histone H4 acetylation (K5, K8, K12 and K16) is an important modification for chromatin structure, with H4K8Ac having no impact on chromatin structure from mitotic prophase to telophase (similar to H4K16Ac), while H4K5Ac and H4K12Ac, are more dynamic (Wako *et al.*, 2003, 2005). A survey of 17 plants species revealed distribution of histone H4K5ac differs between small and large genome species (Feitoza *et al.*, 2017). In most small genomes species (2C < 5 pg), H4K5ac was enriched in late condensing terminal regions but depleted in early condensing regions, while in large genome species, acetylation was more evenly displayed across the chromosome which were also uniformly condensed during the prophase stage.

The condensin complex is another main player in chromosome organization (Hirano *et al.*, 1997), which is probably recruited by H3S10p (Schmiesing *et al.*, 2000). Its basic structure

is given by the heterodimer of Structural Maintenance of Chromosomes (SMC) proteins SMC2 and SMC4, to which condensin I and II specific regulatory subunits associate. Condensin II accesses the cell nucleus before mitosis and its reduction partially reduces early H3 phosphorylation (Ono *et al.*, 2004). Subsequently, condensin I contributes to prophase chromatin compaction.

Similarly, the cohesin complex also contains two SMC subunits (SMC1 and SMC3), that are connected by an α-kleisin subunit (represented by one of the four homologues SYN1–4 in Arabidopsis), which recruits the HEAT repeat containing subunit SCC3. In addition, different proteins regulate cohesion establishment and maintenance (Bolaños-Villegas *et al.*, 2017). Cohesion is established at the onset of S phase and persists until the metaphase-anaphase transition and it is essential to resist the force of the spindle microtubules while chromosomes are aligned at the equatorial plate, allowing their accurate segregation to opposite poles (Fig. 2). At the beginning of anaphase, cohesion is released from chromosomes in two steps (Nasmyth, 2001). During prophase and prometaphase, cohesin is removed from chromosome arms. In the second step, before the onset of anaphase, remaining cohesin is released from centromeres allowing separation of sister chromatids. The PRECOCCIOUS DISSOCIATION OF SISTERS 5 – WING APART LIKE (PDS5-WAPL) complex eliminates cohesion from chromosome arms, whereas EXTRA SPINDLE POLE BODIES 1 (ESP1) separase removes centromeric cohesin via an ubiquitin-dependent cleavage of the α-kleisin in Arabidopsis (Liu and Makaroff, 2006; Pradillo *et al.*, 2015; De *et al.*, 2016). ESP1 is also important for the proper establishment of the radial microtubule network and nuclear/cytoplasmic domains (Yang *et al.*, 2009). Several studies have demonstrated that cohesin plays additional roles in DNA double-strand break repair (DSBR) and regulation of gene expression (Yuan *et al.*, 2011; Mehta *et al.*, 2012).

There are remarkable differences in chromatin condensation and organisation between mitosis and meiosis (Fig. 2). Meiotic chromosome condensation proceeds simultaneously to alignment of homologous chromosomes, programmed DSB formation, repair through homologous recombination (HR), and establishment and dissolution of the synaptonemal complex (SC). These processes are associated with striking morphological changes including dynamic variations in histone PTMs (Nasuda *et al.*, 2005; Oliver *et al.*, 2013). In leptonema, sites of DSB formation and their repair become marked with the γ-H2A.X (Shroff *et al.*, 2004). In pachynema, γ-H2A.X is completely lost from fully synapsed chromosomes. In barley, the first γ-H2A.X foci appeared only four hours after DNA replication in pollen mother cells (PMCs) (Higgins *et al.*, 2012; He *et al.*, 2017). In Arabidopsis, DSB hotspots are also associated with the markers of active chromatin, including histone H2A.Z variant and H3K4me3 modification, low nucleosome density and low DNA methylation (Choi *et al.*, 2013). Similarly, crossovers (COs) reside in genomic regions of "open chromatin", which were identified based on hypersensitivity to DNase I digestion and H3K4me3 enriched nucleosomes in potato (Marand *et al.*, 2017). This is also likely the case for barley as DSBs and H3K4me3 are strongly localized towards the telomeres, whereas they are quite low in pericentromeric

regions (Baker *et al.*, 2015). However, only 20% of the DSBs are effectively associated with H3K4me3, leaving the other 80% unexplained in maize (Sidhu *et al.*, 2015; He *et al.*, 2017).

SWITCH1 (SWI1) is a plant-specific protein that regulates the switch from mitosis to meiosis (Mercier *et al.*, 2001; Agashe *et al.*, 2002; Sheehan and Pawlowski, 2009). Recently, it has been reported that SWI1 antagonizes WAPL during prophase I through a Sororin-like strategy in mitosis (Yang *et al.*, 2019). *swi1* mutants have altered distribution of acetylated histone H3 and dimethylated histone H3 (H3K4me2) (Boateng *et al.*, 2008). Interestingly, H3K4me2 is recognised by MALE MEIOCYTE DEATH 1 (MDD1), a PHD finger protein which acts as a transcriptional regulator, essential for Arabidopsis male meiosis (Andreuzza *et al.*, 2015). Arabidopsis plants defective for ARABIDOPSIS SKP1-LIKE1 (ASK1), a component of the SKP1-CUL1-F-box (SCF) ubiquitin ligase, also displays variations in acetylated histone H3 and H3K9me2 distribution patterns during meiosis (Yang *et al.*, 2006). The influence of these PTMs in meiotic HR has been highlighted in a recent work in which the disruption of H3K9me2 and DNA methylation pathways produce the epigenetic activation of meiotic recombination near centromeres (Underwood *et al.*, 2018; Choi *et al.*, 2018). These are regions normally suppressed for COs in order to avoid aneuploidies in the offspring (Rockmill *et al.*, 2006). In rice, the chromosomes are reprogrammed during the transition to meiosis under the control of the Argonaute protein MEIOSIS ARRESTED AT LEPTOTENE 1 (MEL1), increasing H3K9me2 and decreasing H3K9ac and H3S10p in order to promote synapsis and HR (Liu and Nonomura, 2016).

Entangling of meiotic prophase I chromosomes results in interlocks (Gelei, 1921), which could compromise chromatin integrity and result in chromosome mis-segregation. Here, the organisation and movements of chromosome termini (typically traced by labeling of telomeric repeats) and TOPOISOMERASE II (TOPII) activity are essential for removal of the interlocks (Martinez-Garcia *et al.*, 2018). At the onset of meiosis, telomeres attach to the NE and cluster forming a characteristic bouquet arrangement (Bass *et al.*, 2000). The mechanism of bouquet formation is not well understood and although it is widely conserved among eukaryotes, a characteristic bouquet arrangement is apparently not formed in Arabidopsis (Armstrong *et al.*, 2001). In Arabidopsis, telomeres present a complex behavior and are associated with the nucleolus throughout meiotic interphase and early prophase I. Clustering of telomeres around nucleolus allows pairing at the same time when axial elements of the SC are assembled (Roberts *et al.*, 2009). However, in other species, the subtelomeric regions undergo differential behaviour during premeiotic G2 and prophase I (Colas et al., 2008; Richards et al., 2012). In the large genome of cereals, the telomere bouquet precedes chromosomes synapsis (Phillips *et al.*, 2012; Barakate *et al.*, 2014), and although it is not required for pairing of homologous chromosomes, it may facilitate this process (Golubovskaya *et al.*, 2002). In this context, HR and synapsis start in the distal regions of the chromosomes in barley, but it has been suggested that this is likely related to the heterochromatin/euchromatin replication program rather than the telomere movements (Higgins *et al.*, 2012).

SMC complexes are essential during meiosis. Both condensin I and II complexes are important for maintaining the structure of meiotic chromosomes. Condensin I ensures normal condensation in centromeric and 45S rDNA regions, whereas condensin II eliminates interchromosome connections (Smith *et al.*, 2014). In addition, the cohesin complex is indispensable for proper pairing and HR (Golubovskaya *et al.*, 2006). Several meiosis-specific cohesin proteins have been identified in plants (Bolaños-Villegas *et al.*, 2017), but it is unknown how the replacement of the respective mitotic proteins takes place. ABSENCE OF FIRST MEIOTIC DIVISION 1 (AFD1), the meiosis-specific maize kleisin protein, is required for elongation of axial elements of the synaptonemal complex and also for normal bouquet formation (Golubovskaya *et al.*, 2006). In rice, if centromere cohesion is compromised, chromatids separate prematurely at anaphase I and chromosomes are intertwined, leading to chromosome bridges and fragmentation (Shao *et al.*, 2011). Mutants deficient for Arabidopsis SYNAPTIC 1 (SYN1), a meiosis-specific α-kleisin, present defects in arm cohesion during prophase I and problems in centromere cohesion from anaphase I onwards (Bai *et al.*, 1999; Cai *et al.*, 2003). In order to protect premature SYN1 depletion and thus cohesion at centromeres, SYN1 needs to be dephosphorylated by the protein phosphatases PP2AB'α and PP2AB'β (Yuan *et al.*, 2018). Precocious separation of sister chromatids at centromeres is also avoided by SHUGOSHIN-LIKE 1 and 2 (SGOL1 and SGOL2), and PATRONUS 1 (PANS1) (Cromer et al., 2013; Zamariola et al., 2014). This function is most likely conserved in both mitosis and meiosis as shown in rice (Wang *et al.*, 2011). In Arabidopsis, absence of functional ESTABLISHMENT OF COHESION 1/CHROMOSOME TRANSMISSION FIDELITY 7 (ECO1/CTF7), involved in the establishment of chromatid cohesion, also produces severe reduction of cohesion during meiosis (Bolaños-Villegas *et al.*, 2013). Furthermore, mutations in the two Arabidopsis *WAPL* genes, with a significant role in the removal of cohesin, lead to alterations in the organisation of heterochromatin and delayed cohesin removal during prophase I (De *et al.*, 2014). Concerning the SMC5/6 complex, the SUMO (Small Ubiquitin-like Modifier) E3 ligase activity conferred by METHYL METHANE SULFONATE SENSITIVITY 21 (MMS21) and NSE4A kleisin are required for normal meiotic progression and gametophyte development in Arabidopsis (Liu *et al.*, 2014; Diaz *et al.*, 2019; Zelkowski *et al.*, 2019).

Most of the information on the behavior of chromatin in meiosis derives from studies with fixed cells. However, innovative methodologies are being developed to enable the dynamic analysis of meiotic processes in live meiocytes. In a pioneer study, prophase I has been analyzed within PMCs of intact anthers in maize (Sheehan and Pawlowski, 2009) and recently live microscopy of male meiosis was performed at high resolution in Arabidopsis (Prusicki *et al.*, 2019). Such technology advancements will allowan in-depth analysis of dynamics of meiotic processes. Finally, the link between chromatin conformation and gene regulation during meiosis is still very obscure despite the number of genomic and transcriptomic studies in various plant species (Zhou and Pawlowski, 2014). However, most of these analyses have mainly been done with tissue covering the overall meiosis rather than specific meiotic stages, which is necessary to understand the gene expression pattern. In

addition, transcriptomic studies would also benefit from complementary proteomic experiments to address the regulation of gene/protein meiotic networks.

Chromatin dynamics during reproductive development

In Angiosperms, sexual reproduction starts with the development of flowers, when the SAM is transformed into the inflorescence meristem (IM) continuously producing the floral meristems (FM). Remarkably, the FM switches from an indeterminate fate to a determinate fate to give rise to all the organs of the flower, the gametes and the fruit. All reproductive development transitions are controlled by endogenous, hormonal or external environmental signaling pathways, which require complex gene regulatory networks involving transcription factors and epigenetic mechanisms.

The floral initiation is precisely coordinated via a complex gene network that integrates the age, photoperiod, temperature and hormonal signals (Andres and Coupland, 2012). At favorable conditions, the Arabidopsis systemic floral activator *FLOWERING LOCUS T* (*FT*, the florigen) or its orthologues in other species (e.g. *VRN3* in cereals) change SAM to IM. In Arabidopsis, FT expression is subjected to photoperiod and ambient temperature and is under a complex balance of active and repressive chromatin modifications involving both Polycomb Repressive Complex (PRC) 1 and 2 (He, 2012). Expression of FT target and flowering-pathway integrator, SUPPRESSION OF OVEREXPRESSION OF CONSTANS 1 (SOC1) turns on the FM identity genes *APETALA 1* (*AP1*) and *LEAFY*, which promote the formation of the floral primordium (reviewed in Guo et al., 2015). The homeodomain transcription factor WUSCHEL (WUS) plays a central role in the process of FM determinacy by specifying the maintenance of stem cell activity within the organizing center of SAM, IM and FM (Cao *et al.*, 2015). In cooperation with LEAFY, WUS activates the MADS-box transcription factor *AGAMOUS* (*AG*), which initiates the reproductive organ development. Thereafter, AG represses *WUS* activity to ensure the FM termination, and to promote all the finely tuned developmental transitions required for the proper development of floral organs. The repression of *WUS* is a perfect example to illustrate the importance of epigenetic regulatory mechanisms during FM termination. First, AG binds to the *WUS* locus, which allows the recruitment of the PRC2 catalytic subunit CURLY LEAF to mediate the deposition of H3K27me3 repressive marks on *WUS*. Then components of PRC1 complex recognize the H3K27me3, which results in the compaction of chromatin and further *WUS* repression. Thereafter, AG turns on the C2H2 zinc-finger transcription factor *KNUCKLES* gene (*KNU*), which terminates the inflorescence by stabilizing WUS repression (Bollier *et al.*, 2018).

After meiosis (see the previous chapter), the male haploid gametophyte (microspore) undergoes an asymmetric division to produce a generative cell (GC) and a vegetative cell (VC), and the GC divides once more to produce two sperm cells (SCs) representing the male gametes (reviewed by e.g. Berger and Twell, 2011). SCs and VCs have very different chromatin characteristics, which determine also their fate, genome integrity and capacity to divide (Slotkin *et al.*, 2009; Calarco *et al.*, 2012; Ibarra *et al.*, 2012). The SC nuclei are very compact and strongly repress transposons by maintaining high levels of H3K9me2, CG and CHG

methylation (Schoft *et al.*, 2009; Calarco *et al.*, 2012; Ibarra *et al.*, 2012; Hsieh *et al.*, 2016), whereas CHH methylation is generally low, but shows complex dynamics with temporal increases (Walker *et al.*, 2018). In contrast, the VC nuclei are de-condensed, without CenH3, H3K9me2 and DECREASED IN DNA METHYLATION 1 (DDM1), but rich in 21-nt siRNAs, suggesting loss of competence to divide, strongly reduced maintenance methylation control and activation of the non-canonical RdDM pathway (Schoft *et al.*, 2009; Slotkin *et al.*, 2009; Creasey *et al.*, 2014). This leads to the decreased CG methylation and increased CHH methylation levels and transcriptional activation of TEs in VC (Mosher *et al.*, 2009; Slotkin *et al.*, 2009; Calarco *et al.*, 2012; Creasey *et al.*, 2014; Martínez *et al.*, 2016; Martinez *et al.*, 2018). Furthermore, VCs show enrichment in H3K27me3, indicating high PRC2 activity (Borg and Berger, 2015). Functional significance of such extensive epigenetic reprogramming is still debated, but the activation of TEs in VC may represent a non-autonomous silencing mechanism, which switches off any potentially active transposons in the germline and thus preserves the genome integrity of the next generation. However, to what extent is this typical for plants other than Arabidopsis remains unknown. For example, cereals lack specific epigenetic factors present in Arabidopsis such as DEMETER (DME) or CHROMOMETHYLASE 2 (CMT2), but have multiple copies of other factors including DNA METHYLTRANSFERASE 1 (MET1), CHROMOMETHYLASE 3 (CMT3), DDM1 or specific subunits of Pol IV and Pol V (Zemach *et al.*, 2010, 2013; Li *et al.*, 2014; Haag *et al.*, 2014; Shi *et al.*, 2015; Bewick and Schmitz, 2017). In addition, the same factors in cereals may have different effects on DNA methylation such as ZmDDM1 that is required for the formation of mCHH islands via the RdDM pathway (Long *et al.*, 2018; Fu *et al.*, 2018). All this indicates a diversification and/or specialization of functions and a more important role of the small RNAs in epigenetic programming of cereal pollen. In rice SCs, there is high expression from *OsDRM2* and new small RNA pathway involving a non-canonical ARGONAUTE (AGO) and DICER-LIKE (DCL3) proteins, suggesting high CHH methylation levels (Russell *et al.*, 2012; Anderson *et al.*, 2013). In addition, there seem to be a specific variant of Pol V largest subunit in grasses (Trujillo *et al.*, 2018) and future studies will reveal whether these factors act in a novel RdDM pathway. Long intergenic noncoding RNAs (lincRNAs), correlated with H3K27me3 have been identified in the rice male gametophyte (Zhang *et al.*, 2014; Johnson *et al.*, 2018). Given the high and medium numbers of copies of putative orthologs of H3K27 and H3K4 demethylases, respectively, indicates that rice SCs may require more extensive reprogramming of repressive marks (Anderson *et al.*, 2013).

The replacement of canonical histones by specific variants is also characteristic of epigenetic control at male gametogenesis. In Arabidopsis SCs, the histone H3 variant, MALE GAMETE-SPECIFIC HISTONE 3 (MGH3), is the most abundant (Okada *et al.*, 2005; Ingouff *et al.*, 2007; Ingouff and Berger, 2010). This variant has been correlated with the loss of H3K27me3 methylation, due to the composition of the adjacent amino acid residues (Borg and Berger, 2015). In rice, a specific combination of H2A, H2B and H3 histone proteins has also been identified in SCs (Russell *et al.*, 2012; Anderson *et al.*, 2013). Histone H3.709 and H2A.Z are the most remarkable. Histone H3.709, although probably an ortholog of MGH3, is quite divergent in the amino acid composition. Replacement of histones also occurs in the

Arabidopsis VC, since CenH3 is progressively lost in centromeric heterochromatin when it begins to de-condense, while there is a loss of H3K9me2 marks, indicating a state of terminal differentiation (Schoft *et al.*, 2009; Mérai *et al.*, 2014). However, CenH3 and H3K9me2 persist in VC of rye and barley (Houben *et al.*, 2011; Pandey *et al.*, 2013), probably reflecting a temporal shift between pollination and fertilization in these species (Borg and Berger, 2015). In maize, the haploid microspores carrying a knock-down mutation in *hda108* gene collapsed and failed to develop properly, indicating that histone acetylation/deacetylation affects microspore viability (Forestan *et al.*, 2018). In *Brassica rapa*, H3K4me3 and H3K27me3 deposition is necessary for the regulation of the pollen wall construction (Shen *et al.*, 2019).

Female gametophyte develops in ovule according to the Polygonum type in ~70% of flowering plants, including e.g. Arabidopsis, maize, rice, wheat and soybean. In megasporogenesis, the diploid megaspore mother cell undergoes meiosis resulting in four haploid megaspores. One megaspores develops into the female gametophyte, while the other die. The formation and differentiation of the different cell types in the reproductive lineage are characterized by global changes in chromatin organisation. Histone modifications were observed via cytogenetic and chromatin reporter studies in Arabidopsis megaspore and also in the surrounding nucellar cells in maize (Garcia-Aguilar *et al.*, 2010; She *et al.*, 2010). Genetic analyses have identified DNA methylation acting upon the megaspore fate establishment, and also action of small RNAs silencing transposable elements in the female gametes in Arabidopsis and maize (Garcia-Aguilar *et al.*, 2010; Olmedo-Monfil *et al.*, 2010). The multicellular embryo sac consists of the egg cell, the central cell, two synergid cells and three antipodal cells. The female gametes, exhibit chromatin dimorphism as they express different histone H3 proteins with the egg cell expressing only the H3.3 variant, whereas there are both H3.1 and H3.3 proteins in the central cell (Ingouff and Berger, 2010). Due to the technically limiting accessibility to the female gametophyte, gene level resolution of the chromatin perturbations has not been reported to date. The histone modifications observed, suggest a global epigenetic reprogramming phase during the female gametophyte development. The epigenetic dimorphism of the two female gametes at the DNA methylation level, with the global demethylation of the central cell versus the non-CG DNA methylation of the egg cell highlights the different roles, which these two cell types are going to play in seed development (Pillot *et al.*, 2010). For an extensive review on the dynamics of the chromatin landscape on the female gametophyte development follow Baroux & Autran, (2015).

In the zygote, the parentally derived histone H3 variants are replaced before the first division of the embryo to reflect the content found in sporophytic cells (Ingouff and Berger, 2010). Two maternal epigenetic pathways are acting in the early embryo to regulate the paternal transcripts, the RdDM pathway and the histone chaperone complex Chromatin assembly factor 1 (CAF1). These pathways do not regulate genomic imprinting (Autran *et al.*, 2011). The central cell will give rise (upon fusion with one sperm cell nucleus) to the endosperm. In endosperm, maternally expressed genes will be suppressed by PRC2 complex, including central cell lineage specific H3K27 methyltransferase FERTILIZATION INDEPENDENT SEED 1/MEDEA (FIS1/MEA), implicated in the regulation of type I MADS-box genes and transition

from syncytial to cellularized stage (Zhang et al., 2018). It should be noted that endosperm development is sensitive to parental genome dosage and the majority of imprinted genes reported are expressed from the maternal genome in the endosperm (reviewed in e.g. Gehring and Satyaki, 2017). Endosperm chromatin is characterized by a looser structure, DNA hypomethylation and decreased levels of H3K9me2, when compared to somatic tissues and embryo (Baroux *et al.*, 2007; Pillot *et al.*, 2010). In contrast to embryo development, extensive demethylation occurs during endosperm development and this dynamic process allows for imprinting variation observed in maize and Arabidopsis (Gehring *et al.*, 2009; Waters *et al.*, 2013; Pignatta *et al.*, 2018). In maize, HDA101, and members of different chromatin remodeling complexes affect endosperm transfer cells leading to alteration in the kernel size (Yang *et al.*, 2016). Kernels of *hda108 hda101* plants showed a strong defective phenotype with fully or partially empty pericarp. Starchy endosperm tissue failed to accumulate starch or developed only partially in defective kernels, while the embryo showed abnormalities that varied from the presence of an undifferentiated aborted embryo to a defective embryo blocked at the coleoptilar stage (Forestan *et al.*, 2018).

Seeds are embedded in fruits, many of which are important source of food to humans. The best understood development of fleshy fruits is tomato, which displays remarkable characteristics related to chromosome structure, chromatin organisation and dynamics (Bourdon *et al.*, 2012). A major developmental feature is the increase in nuclear DNA content due to endoreduplication leading to cell hypertrophy, thereby influencing fruit growth and size (Chevalier et al., 2014). Whether chromatin modifications are associated with endoreduplication still remains largely unknown. However, it was shown in Arabidopsis that endoreduplicated nuclei have less condensed heterochromatin (Schubert *et al.*, 2006; Jegu *et al.*, 2013). In tomato, DNA methylation decreases in the highly endoreduplicated pericarp tissue and is significantly reduced at the onset of fruit maturation and during ripening (Teyssier *et al.*, 2008; Zhong *et al.*, 2013), possibly to control the gene expression according to a tissue-specific endoreduplication status**.** Ectopic overexpression of the DAMAGED DNA BINDING PROTEIN 1 (DDB1), member of the DDB1-CUL4-based E3 ubiquitin ligase complex, regulating many developmental processes via chromatin remodeling, decreased the size of flowers and fruits in tomato (Liu *et al.*, 2012) via up-regulation of two positive regulators of endoreduplication *SlWEE1* and *SlCCS52A* (Azzi *et al.*, 2015). Currently, there is increasing evidence for the epigenetic control during fruit organogenesis and epigenome dynamics plays an important role during fruit maturation and ripening in tomato (reviewed in Giovannoni et al., 2017).

Plant chromatin modifications for the purposes of plant breeding

Decades of breeding and selection have narrowed down the pool of genetic variability in many crops (Palmgren *et al.*, 2015). Crop breeding programs have classically relied on sequence-based genetic variability of either natural or induced origin. These efforts have allowed the generation of varieties with an increased and more stable yield, and relatively well adapted to biotic and abiotic stresses. However, the exploitation of genetic variability existing within gene

pools has been limited. Furthermore, not all the heritable phenotypic diversity can be explained by sequence variation and has been termed as the missing heritability (Maher, 2008; Gallusci *et al.*, 2017). Such variation could have epigenetic basis.

Applicability of chromatin modifications for the purpose of crop improvement (Fig. 3) depends on their stability and heritability as the two key features. Epigenetic modifications may be of interest for breeders only if their regulatory effects are maintained through mitosis and ideally through meiosis. Here, DNA methylation and specific histone PTMs are the prime candidates for crop improvement, as they were mitotically transmittable for at least limited time in several species (Hyun *et al.*, 2013; Gaydos *et al.*, 2014; Avramova, 2015; Jiang and Berger, 2017; Kawakatsu *et al.*, 2017). This raises the possibility of employing them as tools for breeding in clonally-propagated crops, e.g. many fruit trees. However, for seed-propagated crops, specific chromatin modifications need to pass the epigenetic resetting barriers during gametogenesis and seed development in order to pass to the next generation (Pecinka and Mittelsten Scheid, 2012; Grossniklaus *et al.*, 2013; Iwasaki and Paszkowski, 2014; Kawashima and Berger, 2014; Quadrana and Colot, 2016; Roessler *et al.*, 2018). Here, DNA methylation seems the best candidate due to its stability and because PTMs are lost due to gametogenesis specific removal and replacement of the parental nucleosomes (Ingouff *et al.*, 2010; Quadrana and Colot, 2016).

Plant developmental processes determine a great number of traits of agronomical interest that have been targeted for selection in crops. Some of them are epigenetically regulated, either by DNA methylation or histone PTMs such as leaf shape, flowering time and flower development, male fertility, oil yield, fruit ripening, grain size, plant stature, inflorescence structure, branching plant architecture, boll setting rate, abscission rate, photoperiod responses, etc. (Zhang, 2012; Ong-Abdullah *et al.*, 2015; Xianwei *et al.*, 2015; Bull *et al.*, 2017; Latrasse *et al.*, 2017*b*; van Esse *et al.*, 2017; Fan *et al.*, 2018; Song *et al.*, 2018). Expanding evidence also shows that epigenetic control has an important role in the fine-tuning of the responses to biotic and abiotic stress (Gourcilleau *et al.*, 2010; Kim *et al.*, 2010; González *et al.*, 2011, 2013; Ding and Wang, 2015). This raises the possibility to generate or select variability of epigenetic changes to assist plant breeding. Stably inherited epialleles have been characterized for genes controlling some developmental processes. Examples of such epialleles in crops include: tomato *CNR* locus controlling fruit ripening (Manning *et al.*, 2006), oil palm *MANTLED* that regulates oil yield (Ong-Abdullah *et al.*, 2015), cotton *CONSTANS-LIKE 2* that determines photoperiod sensibility (Song *et al.*, 2017), rice *FERTLIZATION INDEPENDENT ENDOSPERM 1* (*FIE1*), which regulates plant height and flower development (Zhang *et al.*, 2012), *RAV6* affecting leaf angle and grain size (Xianwei *et al.*, 2015) or *SEMI-ROLLED LEAF 1* (*SRL1*), which determines rice cell wall formation (Li *et al.*, 2017).

Thus, epigenetic modifications are a source of phenotypic diversity and it is desirable to identify and/or generate novel epialleles of interest for crop improvement (Fig. 3). One possible approach is to select epigenetic variants among the natural diversity by exploiting DNA methylation states in different germplasms (Takuno *et al.*, 2016). This type of analysis has revealed large amounts of epigenetic variability in ecotypes, cultivars, landraces and wild

relatives (Eichten *et al.*, 2013; Schmitz *et al.*, 2013*b*; Garg *et al.*, 2015; Venetsky *et al.*, 2015; Kumar *et al.*, 2017; Song *et al.*, 2017; Liu *et al.*, 2018; Shen *et al.*, 2018). However, it requires good reference genomes and can be more time-consuming and tedious than mining genetic polymorphisms. The easiest way to link DNA methylation polymorphisms with phenotypes is to simultaneously monitor gene expression (Eichten *et al.*, 2013; Song *et al.*, 2017). However, this may be challenging for genes with tissue specific transcription.

Epialleles can be also generated artificially. Untargeted approaches employ cell culture (Mittelsten Scheid *et al.*, 2003; Ong-Abdullah *et al.*, 2015; Li *et al.*, 2017; Coronel *et al.*, 2018), abiotic stresses (Verkest *et al.*, 2015), transposon mobilization (Thieme *et al.*, 2017), or treatment with specific epigenetic inhibitors (Marfil *et al.*, 2012; Baubec *et al.*, 2014; Pecinka and Liu, 2014; Xu *et al.*, 2016; Zhu *et al.*, 2018). In addition, this can be achieved by the generation of epigenetic recombinant inbred lines (epiRILs) from crosses between wild type and maintenance DNA methylation mutants. Although epiRILs are a well-established system in Arabidopsis (Dapp *et al.*, 2015; Zhang *et al.*, 2016; Lauss *et al.*, 2018; Zhang *et al.*, 2018*a*), their use in crops is still in its infancy and might be influenced by the reproductive modality (Schmitz *et al.*, 2013*a*) and availability of viable epiregulator mutants (Anderson *et al.*, 2018). However, the current trends are directed towards controlled induction of the chromatin states. The RNA interference (RNAi) allows directing DNA methylation to specific positions and thus silencing the target loci. In addition, there are first studies demonstrating that modified CRISPR system using Cas9 or related nucleases (such as Cfp1) offer wide possibilities to change chromatin at specific loci (Liu and Moschou, 2018; Xie *et al.*, 2018). In this approach, chromatin remodelers, DNA or histone (de)methylases, transcription factors or specific protein domains can be, directly or via a marker peptide-antibody based system, fused to the catalytically dead Cas9 (dCas9), which leads to the recruitment of dCas9 to the locus of interest and chromatin change (Liu and Moschou, 2018; Xie *et al.*, 2018; Gallego-Bartolomé *et al.*, 2018). We predict that the number of dCas9 induced modifications will grow rapidly in the model plants as well as in crops. This approach has a great potential to shed more light on how the chromatin states are established, maintained and erased in plants. In addition, this could improve agriculturally relevant developmental or stress resistance-related traits in crops; however, the legal restrictions will most likely remain the main hurdle towards practical use of such inventions world-wide.

Chromatin modifications have emerged as a complementary source of variability contributing to plant phenotypic plasticity (Fig. 3). It could also address new challenges in crop improvement, including adaptive responses to environmental stresses. Since the emergence and inheritance of epigenetic variation differs from the genetic variants, current methods of trait mapping miss substantial phenotype-determining variation and thus may have reduced efficacy. Therefore, the relative contribution of genetic versus epigenetic variation remains unknown (Pecinka *et al.*, 2013). However, plant breeding using chromatin traits can be assisted by newly developed tools including process-based models (Hu *et al.*, 2015; Gallusci *et al.*, 2017), or epigenome-wide association studies (EWAS) (Rakyan *et al.*, 2011).

Future perspectives in plant breeding strategies

Classical plant breeding harnesses the genetic variation that is generated by homologous recombination during meiosis. For example, in cereals, a high amount of 20-30% (according to some sources up to 50%) of genes rarely recombine (Sandhu and Gill, 2002; The International Barley Sequencing Consortium, 2012; Higgins et al., 2014; Mascher et al., 2017), limiting the genetic diversity available for plant breeders and breaking the desirable combination of alleles in elite cultivars (Mascher *et al.*, 2017; Appels *et al.*, 2018; Ramírez-González *et al.*, 2018). In this context, a better understanding about the influence of the epigenetic makeup on meiotic recombination would contribute to development of novel strategies to modify the recombination pattern and to generate new elite crop varieties (Fig. 3). The ever increasing knowledge drawn from epigenetics studies in model and crop plants paves the way to applied perspectives and foreseen plant breeding strategies. The exploitation of epigenetic diversity is the forthcoming challenge for next plant breeding strategies, since chromatin modifications are tightly intertwined with plant phenotypic plasticity (reviewed in Pecinka et al., 2013; Gallusci et al., 2017). To cope with the improvement of genetic diversity resulting from intense plant breeding programs, epigenetic diversity may thus provide this opportunity to select for new traits related to plant adaptation to environmental constraints, crop yield or quality of plant products, pending a better understanding of all the associated regulatory mechanisms.

Acknowledgements

The work of all authors on this manuscript was stimulated and supported by the COST action CA16212 “Impact of Nuclear Domains On Gene Expression and Plant Traits”. A.P. was supported from ERDF project "Plants as a tool for sustainable global development" (No. CZ.02.1.01/0.0/0.0/16_019/0000827), INTER-COST grant LTC18026 from the MEYS Czech Republic and Purkyně Fellowship from the Czech Academy of Sciences. C.C. was supported by the EU Horizon 2020 project TomGEM (N°. 679796). I.C. was supported by the European Research Council Shuffle (ERC-Advanced to Prof. R. Waugh; Project ID: 669182). K.K. was supported by a grant of the General Secretary for Research and Technology of Greece, Infrastructures support program [MIS5002803] "PlantUP". S.V. was supported by Italian CNR Epigen Flagship Project. T.K. was supported by the US-Israel Binational Agricultural Research and Development Fund (US 4916-16). C.M. was supported from the ERDF project “Centre for Experimental Plant Biology” (No. CZ.02.1.01/0.0/0.0/16_019/0000738), grants from the MEYS Czech Republic (LTC18034) and the Czech Science Foundation (18-02448S). M.-P.V. was supported by the project AGL2016-77211-R from ‘Plan Nacional de Recursos y Tecnologías Agroalimentarias’ of Spain. A.M. was supported by the Spanish Ministry of Economy and Competitiveness (MINECO) and Fondo Europeo de Desarrollo Regional (FEDER grant BIO2014-57011-R). M.P. acknowledges support from the Spanish Ministry of Economy and Competitiveness (MINECO) (AGL2015-67349-P) and Horizon 2020 Programme (Marie-Curie ITN MEICOM network FP7 ITN-765212).

References

Agashe B, Prasad CK, Siddiqi I. 2002. Identification and analysis of DYAD: a gene required for meiotic chromosome organisation and female meiotic progression in Arabidopsis. Development **129**, 3935–3943.

Anderson SN, Johnson CS, Jones DS, Conrad LJ, Gou X, Russell SD, Sundaresan V. 2013. Transcriptomes of isolated Oryza sativa gametes characterized by deep sequencing: evidence for distinct sex-dependent chromatin and epigenetic states before fertilization. Plant Journal **76**, 729–741.

Anderson SN, Zynda GJ, Song J, Han Z, Vaughn MW, Li Q, Springer NM. 2018. Subtle perturbations of the maize methylome reveal genes and transposons silenced by Chromomethylase or RNA-directed DNA methylation pathways. G3: Genes|Genomes|Genetics **8**, 1921–1932.

Andres F, Coupland G. 2012. The genetic basis of flowering responses to seasonal cues. Nature Reviews Genetics **13**, 627–639.

Andreuzza S, Nishal B, Singh A, Siddiqi I. 2015. The chromatin protein DUET/MMD1 controls expression of the meiotic gene TDM1 during male meiosis in Arabidopsis. PLOS Genetics **11**, e1005396.

Appels R, Eversole K, Feuillet C, *et al.* 2018. Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science **361**, eaar7191.

Armstrong SJ, Franklin FCH, Jones GH. 2001. Nucleolus-associated telomere clustering and pairing precede meiotic chromosome synapsis in Arabidopsis thaliana. Journal of Cell Science **114**, 4207–4217.

Autran D, Baroux C, Raissig MT, *et al.* 2011. Maternal epigenetic pathways control parental contributions to Arabidopsis early embryogenesis. Cell **145**, 707–719.

Avramova Z. 2015. Transcriptional 'memory' of a stress: transient chromatin and memory (epigenetic) marks at stress-response genes. Plant Journal **83**, 149–159.

Azzi L, Deluche C, Gévaudant F, Frangne N, Delmas F, Hernould M, Chevalier C. 2015. Fruit growth-related genes in tomato. Journal of Experimental Botany **66**, 1075–1086.

Bai X, Peirson BN, Dong F, Xue C, Makaroff CA. 1999. Isolation and characterization of SYN1, a RAD21-like gene essential for meiosis in Arabidopsis. Plant Cell **11**, 417–430.

Baker K, Dhillon T, Colas I, Cook N, Milne I, Milne L, Bayer M, Flavell AJ. 2015. Chromatin state analysis of the barley epigenome reveals a higher-order structure defined by H3K27me1 and H3K27me3 abundance. Plant Journal **84**, 111–124.

Barakate A, Higgins JD, Vivera S, *et al.* 2014. The synaptonemal complex protein ZYP1 is required for imposition of meiotic crossovers in barley. Plant Cell **26**, 729–740.

Baroux C, Autran D. 2015. Chromatin dynamics during cellular differentiation in the female reproductive lineage of flowering plants. Plant Journal **83**, 160–176.

Baroux C, Pien S, Grossniklaus U. 2007. Chromatin modification and remodeling during early seed development. Current Opinion in Genetics and Development **17**, 473–479.

Bass HW, Riera-Lizarazu O, Ananiev E V, Bordoli SJ, Rines HW, Phillips RL, Sedat JW, Agard DA, Cande WZ. 2000. Evidence for the coincident initiation of homolog pairing and synapsis during the telomere-clustering (bouquet) stage of meiotic prophase. Journal of Cell Science **113**, 1033–1042.

Baubec T, Finke A, Mittelsten Scheid O, Pecinka A. 2014. Meristem-specific expression of epigenetic regulators safeguards transposon silencing in Arabidopsis. EMBO Reports **15**, 446–452.

Berger F, Twell D. 2011. Germline specification and function in plants. Annual Review of Plant Biology **62**, 461–484.
Bewick AJ, Schmitz RJ. 2017. Gene body DNA methylation in plants. Current Opinion in Plant Biology **36**, 103–110.
Boateng KA, Yang X, Dong F, Owen HA, Makaroff CA. 2008. SWI1 is required for meiotic chromosome remodeling events. Molecular Plant **1**, 620–633.
Boden SA, Kavanová M, Finnegan EJ, Wigge PA. 2013. Thermal stress effects on grain yield in Brachypodium distachyon occur via H2A.Z-nucleosomes. Genome Biology **14**, R65.
Bolaños-Villegas P, De K, Pradillo M, Liu DS, Makaroff CA. 2017. In favor of establishment: Regulation of chromatid cohesion in plants. Front Plant Sci **8**, 846.
Bolaños-Villegas P, Yang X, Wang H-J, Juan C-T, Chuang M-H, Makaroff CA, Jauh G-Y. 2013. Arabidopsis CHROMOSOME TRANSMISSION FIDELITY 7 (AtCTF7/ECO1) is required for DNA repair, mitosis and meiosis. Plant Journal **75**, 927–940.
Bollier N, Sicard A, Leblond J, *et al.* 2018. At-MINI ZINC FINGER2 and SI-INHIBITOR OF MERISTEM ACTIVITY, a conserved missing link in the regulation of floral meristem termination in Arabidopsis and tomato. Plant Cell **30**, 83–100.
Borg M, Berger F. 2015. Chromatin remodelling during male gametophyte development. Plant Journal **83**, 177–188.
Bourbousse C, Mestiri I, Zabulon G, Bourge M, Formiggini F, Koini MA, Brown SC, Fransz P, Bowler C, Barneche F. 2015. Light signaling controls nuclear architecture reorganization during seedling establishment. Proceedins of the National Academy of Sciences U.S.A. **112**, E2836–E2844.
Bourdon M, Pirrello J, Cheniclet C, *et al.* 2012. Evidence for karyoplasmic homeostasis during endoreduplication and a ploidy-dependent increase in gene transcription during tomato fruit growth. Development **139**, 3817–3826.
Bull H, Casao MC, Zwirek M, *et al.* 2017. Barley SIX-ROWED SPIKE3 encodes a putative Jumonji C-type H3K9me2/me3 demethylase that represses lateral spikelet fertility. Nature Communications **8**, 936.
Cai X, Dong F, Edelmann RE, Makaroff CA. 2003. The Arabidopsis SYN1 cohesin protein is required for sister chromatid arm cohesion and homologous chromosome pairing. Journal of Cell Science **116**, 2999–3007.
Calarco JP, Borges F, Donoghue MTA, *et al.* 2012. Reprogramming of DNA methylation in pollen guides epigenetic inheritance via small RNA. Cell **151**, 194–205.
Cao X, He Z, Guo L, Liu X. 2015. Epigenetic mechanisms are critical for the regulation of WUSCHEL expression in floral meristems. Plant Physiology **168**, 1189–1196.
Casati P, Campi M, Chu F, Suzuki N, Maltby D, Guan S, Burlingame AL, Walbot V. 2008. Histone acetylation and chromatin remodeling are required for UV-B-dependent transcriptional activation of regulated genes in maize. Plant Cell **20**, 827–842.
Casati P, Stapleton AE, Blum JE, Walbot V. 2006. Genome-wide analysis of high-altitude maize and gene knockdown stocks implicates chromatin remodeling proteins in response to UV-B. Plant Journal **46**, 613–627.
Cavrak V V, Lettner N, Jamge S, Kosarewicz A, Bayer LM, Mittelsten Scheid O. 2014. How a retrotransposon exploits the plant's heat stress response for its activation. PLoS Genet **10**, e1004115.
Chevalier C, Bourdon M, Pirrello J, Cheniclet C, Gévaudant F, Frangne N. 2014. Endoreduplication and fruit growth in tomato: evidence in favour of the karyoplasmic ratio theory. Journal of Experimental Botany **65**, 2731–2746.

Choi SM, Song HR, Han SK, Han M, Kim CY, Park J. 2012. HDA19 is required for the repression of salicylic acid biosynthesis and salicylic acid-mediated defense responses in Arabidopsis. Plant Journal **71**, 135–146.
Choi K, Zhao X, Kelly KA, *et al.* 2013. Arabidopsis meiotic crossover hot spots overlap with H2A.Z nucleosomes at gene promoters. Nature Genetics **45**, 1327–1336.
Choi K, Zhao X, Tock AJ, *et al.* 2018. Nucleosomes and DNA methylation shape meiotic DSB frequency in Arabidopsis thaliana transposons and gene regulatory regions. Genome Research **28**, 532–546.
Colas I, Shaw P, Prieto P, Wanous M, Spielmeyer W, Mago R, Moore G. 2008. Effective chromosome pairing requires chromatin remodeling at the onset of meiosis. Proceedins of the National Academy of Sciences U.S.A. **105**, 6075–6080.
Coleman-Derr D, Zilberman D. 2012. Deposition of histone variant H2A.Z within gene bodies regulates responsive genes. PLoS Genet **8**, e1002988.
Consortium TIBG. 2012. A physical, genetic and functional sequence assembly of the barley genome. Nature **491**, 711–716.
Coronel CJ, González AI, Ruiz ML, Polanco C. 2018. Analysis of somaclonal variation in transgenic and regenerated plants of Arabidopsis thaliana using methylation related metAFLP and TMD markers. Plant Cell Reports **37**, 137–152.
Creasey KM, Zhai J, Borges F, Van Ex F, Regulski M, Meyers BC, Martienssen RA. 2014. miRNAs trigger widespread epigenetically activated siRNAs from transposons in Arabidopsis. Nature **508**, 411–415.
Cromer L, Jolivet S, Horlow C, Chelysheva L, Heyman J, De Jaeger G, Koncz C, De Veylder L, Mercier R. 2013. Centromeric cohesion is protected twice at meiosis, by SHUGOSHINs at anaphase I and by PATRONUS at interkinesis. Current Biology **23**, 2090–2099.
Dapp M, Reinders J, Bédiée A, Balsera C, Bucher E, Theiler G, Granier C, Paszkowski J. 2015. Heterosis and inbreeding depression of epigenetic Arabidopsis hybrids. Nature Plants **1**, 15092.
De K, Bolaños-Villegas P, Mitra S, Yang X, Homan G, Jauh G-Y, Makaroff CA. 2016. The opposing actions of Arabidopsis CHROMOSOME TRANSMISSION FIDELITY7 and WINGS APART-LIKE1 and 2 differ in mitotic and meiotic cells. Plant Cell **28**, 521–536.
De K, Sterle L, Krueger L, Yang X, Makaroff CA. 2014. Arabidopsis thaliana WAPL is essential for the prophase removal of cohesin during meiosis. PLOS Genetics **10**, e1004497.
Dhawan R, Luo H, Foerster AM, Abuqamar S, Du HN, Briggs SD, Mittelsten Scheid O, Mengiste T. 2009. HISTONE MONOUBIQUITINATION1 interacts with a subunit of the mediator complex and regulates defense against necrotrophic fungal pathogens in Arabidopsis. Plant Cell **21**, 1000–1019.
Diallo AO, Ali-Benali MA, Badawi M, Houde M, Sarhan F. 2012. Expression of vernalization responsive genes in wheat is associated with histone H3 trimethylation. Molecular Genetics and Genomics **287**, 575–590.
Diaz M, Pecinkova P, Nowicka A, Baroux C, Sakamoto T, Yuliani Gandha P, Jeřábková H, Matsunaga S, Grossniklaus U, Pecinka A. 2019. SMC5/6 complex subunit NSE4A is involved in DNA damage repair and seed development in Arabidopsis. Plant Cell **31**, 1579–1597.
Ding Y, Fromm M, Avramova Z. 2012. Multiple exposures to drought 'train' transcriptional responses in Arabidopsis. Nature Communications **3**, 740.
Ding B, Wang G-L. 2015. Chromatin versus pathogens: the function of epigenetics in plant immunity. Frontiers in Plant Science **6**, 675.
Dixon JR, Gorkin DU, Ren B. 2016. Chromatin domains: The unit of chromosome

organization. Molecular Cell **62**, 668–680.
Doğan ES, Liu C. 2018. Three-dimensional chromatin packing and positioning of plant genomes. Nature Plants **4**, 521–529.
Dong Q, Li N, Li X, *et al.* 2018. Genome-wide Hi-C analysis reveals extensive hierarchical chromatin interactions in rice. Plant Journal **94**, 1141–1156.
Du J, Zhong X, Bernatavichute Y V, *et al.* 2012. Dual binding of chromomethylase domains to H3K9me2-containing nucleosomes directs DNA methylation in plants. Cell **151**, 167–180.
Dutta A, Choudhary P, Caruana J, Raina R. 2017. JMJ27, an Arabidopsis H3K9 histone demethylase, modulates defense against Pseudomonas syringae and flowering time. Plant Journal **91**, 1015–1028.
Edgar BA, Orr-Weaver TL. 2001. Endoreplication cell cycles. Cell **105**, 297–306.
Edmondson DG, Davie JK, Zhou J, Mirnikjoo B, Tatchell K, Dent SYR. 2002. Site-specific loss of acetylation upon phosphorylation of histone H3. Journal of Biological Chemistry **277**, 29496–29502.
Eichten SR, Briskine R, Song J, *et al.* 2013. Epigenetic and genetic influences on variation in maize populations. Plant Cell **25**, 2783–2797.
Eichten SR, Springer NM. 2015. Minimal evidence for consistent changes in maize DNA methylation patterns following environmental stress. Frontiers in Plant Science **6**, 308.
van Esse GW, Walla A, Finke A, Koornneef M, Pecinka A, von Korff M. 2017. Six-rowed spike 3 (VRS3) is a histone demethylase that controls lateral spikelet development in barley. Plant Physiology **174**, 2397–2408.
Fan S, Wang J, Lei C, Gao C, Yang Y, Li Y, An N, Zhang D, Han M. 2018. Identification and characterization of histone modification gene family reveal their critical responses to flower induction in apple. Biology **18**, 173.
Feitoza L, Costa L, Guerra M. 2017. Condensation patterns of prophase/prometaphase chromosome are correlated with H4K5 histone acetylation and genomic DNA contents in plants. PLOS ONE **12**, e0183341.
Feng C-M, Qiu Y, Van Buskirk EK, Yang EJ, Chen M. 2014. Light-regulated gene repositioning in Arabidopsis. Nature Communications **5**, 3027.
Forestan C, Farinati S, Rouster J, Lassagne H, Lauria M, Dal Ferro N, Varotto S. 2018. Control of maize vegetative and reproductive development, fertility, and rRNAs silencing by HISTONE DEACETYLASE 108. Genetics **208**, 1443–1466.
Fransz P, de Jong JH, Lysak M, Castiglione MR, Schubert I. 2002. Interphase chromosomes in Arabidopsis are organized as well defined chromocenters from which euchromatin loops emanate. Proceedins of the National Academy of Sciences U.S.A. **99**, 14584–14589.
Friesner JD, Liu B, Culligan K, Britt AB. 2005. Ionizing radiation–dependent γ-H2AX focus formation requires Ataxia Telangiectasia Mutated and Ataxia Telangiectasia Mutated and Rad3-related. Molecular Biology of the Cell **16**, 2566–2576.
Fu F-F, Dawe RK, Gent JI. 2018. Loss of RNA-directed DNA methylation in maize chromomethylase and DDM1-type nucleosome remodeler mutants. Plant Cell **30**, 1617–1627.
Fu Y, Luo G-Z, Chen K, *et al.* 2015. N6-methyldeoxyadenosine marks active transcription start sites in Chlamydomonas. Cell **161**, 879–892.
Gallego-Bartolomé J, Gardiner J, Liu W, Papikian A, Ghoshal B, Kuo HY, Zhao JM-C, Segal DJ, Jacobsen SE. 2018. Targeted DNA demethylation of the Arabidopsis genome using the human TET1 catalytic domain. Proceedings of the National Academy of Sciences of the United States of America **115**, E2125–E2134.

Gallusci P, Dai Z, Génard M, Gauffretau A, Leblanc-Fournier N, Richard-Molard C, Vile D, Brunel-Muguet S. 2017. Epigenetics for plant improvement: Current knowledge and modeling avenues. Trends in Plant Science **22**, 610–623.
Ganguly DR, Crisp PA, Eichten SR, Pogson BJ. 2017. The Arabidopsis DNA methylome is stable under transgenerational drought stress. Plant Physiology **175**, 1893–1912.
Garcia-Aguilar M, Michaud C, Leblanc O, Grimanelli D. 2010. Inactivation of a DNA methylation pathway in maize reproductive organs results in apomixis-like phenotypes. Plant Cell **22**, 3249.
Garg R, Narayana Chevala C V, Shankar R, Jain M. 2015. Divergent DNA methylation patterns associated with gene expression in rice cultivars with contrasting drought and salinity stress response. Scientific Reports **5**, 1–16.
Gaydos LJ, Wang W, Strome S. 2014. H3K27me and PRC2 transmit a memory of repression across generations and during development. Science **345**, 1515–1518.
Gehring M, Bubb KL, Henikoff S. 2009. Extensive demethylation of repetitive elements during seed development underlies gene imprinting. Science (New York, N.Y.) **324**, 1447–1451.
Gehring M, Satyaki PR. 2017. Endosperm and Imprinting, Inextricably Linked. Plant Physiology **173**, 143 LP – 154.
Gelei J. 1921. Weitere Studien uber die Oogenese des Dendrocoelum lactum. Archiv fur Zellforschung **16**, 88–169.
Giovannoni J, Nguyen C, Ampofo B, Zhong S, Fei Z. 2017. The epigenome and transcriptional dynamics of fruit ripening. Annual Review of Plant Biology **68**, 61–84.
Glazebrook J. 2005. Contrasting mechanisms of defense against biotrophic and necrotrophic pathogens. Annual Review of Phytopathology **43**, 205–227.
Golubovskaya IN, Hamant O, Timofejeva L, Wang C-JR, Braun D, Meeley R, Cande WZ. 2006. Alleles of afd1 dissect REC8 functions during meiotic prophase I. Journal of Cell Science **119**, 3306–3315.
Golubovskaya IN, Harper LC, Pawlowski WP, Schichnes D, Cande WZ. 2002. The pam1 gene is required for meiotic bouquet formation and efficient homologous synapsis in maize (Zea mays L.). Genetics **162**, 1979–1993.
González RM, Ricardi MM, Iusem ND. 2011. Atypical epigenetic mark in an atypical location: cytosine methylation at asymmetric (CNN) sites within the body of a non-repetitive tomato gene. BMC Plant Biology **11**, 1–11.
González RM, Ricardi MM, Iusem ND. 2013. Epigenetic marks in an adaptive water stress-responsive gene in tomato roots under normal and drought conditions. Epigenetics **8**, 864–872.
Gourcilleau D, Bogeat-Triboulot M-B, Le Thiec D, Lafon-Placette C, Delaunay A, El-Soud WA, Brignolas F, Maury S. 2010. DNA methylation and histone acetylation: genotypic variations in hybrid poplars, impact of water deficit and relationships with productivity. Annals of Forest Science **67**, 208.
Grob S, Schmid MW, Grossniklaus U. 2014. Hi-C Analysis in Arabidopsis Identifies the KNOT, a Structure with Similarities to the flamenco Locus of Drosophila. Molecular Cell **55**, 678–693.
Grossniklaus U, Kelly WG, Ferguson-Smith AC, Pembrey M, Lindquist S. 2013. Transgenerational epigenetic inheritance: how important is it? Nature Reviews Genetics **14**, 228–235.
Guo S, Sun B, Looi L-S, Xu Y, Gan E-S, Huang J, Ito T. 2015. Co-ordination of flower

development through epigenetic regulation in two model species: rice and Arabidopsis. Plant and Cell Physiology **56**, 830–842.
Haag JR, Brower-Toland B, Krieger EK, *et al.* 2014. Functional diversification of maize RNA polymerase IV and V subtypes via alternative catalytic subunits. Cell Reports **9**, 378–390.
Hamant O, Golubovskaya I, Meeley R, Fiume E, Timofejeva L, Schleiffer A, Nasmyth K, Cande WZ. 2005. A REC8-dependent plant Shugoshin is required for maintenance of centromeric cohesion during meiosis and has no mitotic functions. Current Biology **15**, 948–954.
He Y. 2012. Chromatin regulation of flowering. Trends in Plant Science **17**, 556–562.
He Y, Wang M, Dukowic-Schulze S, *et al.* 2017. Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. Proceedings of the National Academy of Sciences of the United States of America **114**, 12231–12236.
Heitz E. 1928. Das Heterochromatin der Moose. Jahrbücher für wissenschaftliche Botanik **69**, 762 – 818.
Higgins JD, Osman K, Jones GH, Franklin FCH. 2014. Factors underlying restricted crossover localization in barley meiosis. Annual Review of Genetics **48**, 29–47.
Higgins JD, Perry RM, Barakate A, Ramsay L, Waugh R, Halpin C, Armstrong SJ, Franklin FCH. 2012. Spatiotemporal asymmetry of the meiotic program underlies the predominantly distal distribution of meiotic crossovers in barley. Plant Cell **24**, 4096–4109.
Hirano T, Kobayashi R, Hirano M. 1997. Condensins, chromosome condensation protein complexes containing XCAP-C, XCAP-E and a Xenopus Homolog of the Drosophila Barren protein. Cell **89**, 511–521.
Houben A, Kumke K, Nagaki K, Hause G. 2011. CENH3 distribution and differential chromatin modifications during pollen development in rye (Secale cereale L.). Chromosome Research **19**, 471–480.
Houben A, Wako T, Furushima-Shimogawara R, Presting G, Künzel G, Schubert I, Fukui K. 2002. The cell cycle dependent phosphorylation of histone H3 is correlated with the condensation of plant mitotic chromosomes. Plant Journal **18**, 675–679.
Hsieh P-H, He S, Buttress T, Gao H, Couchman M, Fischer RL, Zilberman D, Feng X. 2016. Arabidopsis male sexual lineage exhibits more robust maintenance of CG methylation than somatic tissues. Proceedings of the National Academy of Sciences of the United States of America **113**, 15132–15137.
Hu Y, Morota G, Rosa GJM, Gianola D. 2015. Prediction of plant height in Arabidopsis thaliana using DNA methylation data. Genetics **201**, 779–793.
Hurel A, Phillips D, Vrielynck N, Mézard C, Grelon M, Christophorou N. 2018. A cytological approach to studying meiotic recombination and chromosome dynamics in Arabidopsis thaliana male meiocytes in three dimensions. Plant Journal **95**, 385–396.
Hyun Y, Yun H, Park K, Ohr H, Lee O, Kim DH, Sung S, Choi Y. 2013. The catalytic subunit of polymerase α ensures stable maintenance of histone modification. Development **140**, 156–166.
Ibarra CA, Feng X, Schoft VK, *et al.* 2012. Active DNA demethylation in plant companion cells reinforces transposon methylation in gametes. Science **337**, 1360–1364.
Ingouff M, Berger F. 2010. Histone3 variants in plants. Chromosoma **119**, 27–33.
Ingouff M, Hamamura Y, Gourgues M, Higashiyama T, Berger F. 2007. Distinct dynamics of HISTONE3 variants between the two fertilization products in plants. Current Biology **17**, 1032–1037.
Ingouff M, Rademacher S, Holec S, Soljić L, Xin N, Readshaw A, Foo SH, Lahouze B, Sprunck

S, Berger F. 2010. Zygotic resetting of the HISTONE 3 variant repertoire participates in epigenetic reprogramming in arabidopsis. Current Biology **20**, 2137–2143.
Ito H, Gaubert H, Bucher E, Mirouze M, Vaillant I, Paszkowski J. 2011. An siRNA pathway prevents transgenerational retrotransposition in plants subjected to stress. Nature **472**, 115–119.
Iwasaki M, Paszkowski J. 2014. Epigenetic memory in plants. EMBO Journal **33**, 1987–1998.
Jablonka E, Raz G. 2009. Transgenerational epigenetic inheritance: Prevalence, mechanisms, and implications for the study of heredity and evolution. The Quarterly Review of Biology **84**, 131–176.
Jackel JN, Storer JM, Coursey T, Bisaro DM. 2016. Arabidopsis RNA polymerases IV and V are required to establish H3K9 methylation, but not cytosine methylation, on geminivirus chromatin. Journal of Virology **90**, 7529–7540.
Jegu T, Latrasse D, Delarue M, *et al.* 2013. Multiple functions of Kip-Related Protein5 connect endoreduplication and cell elongation. Plant Physiology **161**, 1694–1705.
Jiang D, Berger F. 2017. DNA replication-coupled histone modification maitains Polycomb gene silencing in plants. Science (New York, N.Y.) **357**, 1146–1149.
Johnson C, Conrad LJ, Patel R, Anderson S, Li C, Pereira A, Sundaresan V. 2018. Reproductive long intergenic noncoding RNAs exhibit male gamete specificity and Polycomb Repressive Complex 2-mediated repression. Plant Physiology **177**, 1198–1217.
Karimi-Ashtiyani R, Ishii T, Niessen M, *et al.* 2015. Point mutation impairs centromeric CENH3 loading and induces haploid plants. Proceedings of the National Academy of Sciences of the United States of America **112**, 11211–11216.
Kaszas E, Cande WZ. 2000. Phosphorylation of histone H3 is correlated with changes in the maintenance of sister chromatid cohesion during meiosis in maize, rather than the condensation of the chromatin. Journal of Cell Science **113**, 3217–3226.
Kawakatsu T, Nery JR, Castanon R, Ecker JR. 2017. Dynamic DNA methylation reconfiguration during seed development and germination. Genome Biology **18**, 171.
Kawashima T, Berger F. 2014. Epigenetic reprogramming in plant sexual reproduction. Nature Reviews Genetics **15**, 613–624.
Kim J-M, To TK, Nishioka T, Seki M. 2010. Chromatin regulation functions in plant abiotic stress responses. Plant, Cell & Environment **33**, 604–611.
Kotak S, Larkindale J, Lee U, von Koskull-Döring P, Vierling E, Scharf K-D. 2007. Complexity of the heat stress response in plants. Current Opinion in Plant Biology **10**, 310–316.
Koyama M, Kurumizaka H. 2018. Structural diversity of the nucleosome. Journal of Biochemistry **163**, 85–95.
Kumar S, Beena AS, Awana M, Singh A. 2017. Salt-induced tissue-specific cytosine methylation downregulates expression of in contrasting wheat (Triticum aestivum L.) genotypes. DNA and Cell Biology **36**, 283–294.
Kumar SV, Wigge PA. 2010. H2A.Z-containing nucleosomes mediate the thermosensory response in Arabidopsis. Cell **140**, 136–147.
Kwon HJ, Kim JH, Kim M, Lee JK, Hwang WS, Kim DY. 2003. Anti-parasitic activity of depudecin on Neospora caninum via the inhibition of histone deacetylase. Veterinary Parasitology **112**, 269–276.
Lämke J, Bäurle I. 2017. Epigenetic and chromatin-based mechanisms in environmental stress adaptation and stress memory in plants. Genome Biology **18**, 124.
Latrasse D, Jegu T, Li H, *et al.* 2017*a*. MAPK-triggered chromatin reprogramming by histone deacetylase in plant innate immunity. Genome Biology **18**, 131.

Latrasse D, Rodriguez-Granados NY, Veluchamy A, *et al.* 2017*b*. The quest for epigenetic regulation underlying unisexual flower development in Cucumis melo. Epigenetics and Chromatin **10**, 1–17.
Lauss K, Wardenaar R, Oka R, van Hulten MHA, Guryev V, Keurentjes JJB, Stam M, Johannes F. 2018. Parental states are associated with heterosis in epigenetic hybrids. Plant Physiology **176**, 1627–1645.
Law JA, Jacobsen SE. 2010. Establishing, maintaining and modifying DNA methylation patterns in plants and animals. Nature Reviews Genetics **11**, 204–220.
Lermontova I, Rutten T, Schubert I. 2011. Deposition, turnover, and release of CENH3 at Arabidopsis centromeres. Chromosoma **120**, 633–640.
Li G, Wang D, Yang R, *et al.* 2014. Temporal patterns of gene expression in developing maize endosperm identified through transcriptome sequencing. Proceedings of the National Academy of Sciences of the United States of America **111**, 7582–7587.
Li WQ, Zhang MJ, Gan PF, *et al.* 2017. CLD1 / SRL1 modulates leaf rolling by affecting cell wall formation, epidermis integrity and water homeostasis in rice. Plant Journal **92**, 904–923.
Liu C, Cheng Y-J, Wang J-W, Weigel D. 2017. Prominent topologically associated domains differentiate global chromatin packing in rice from Arabidopsis. Nature Plants **3**, 742–748.
Liu Z, Makaroff CA. 2006. Arabidopsis separase AESP is essential for embryo development and the release of cohesin during meiosis. Plant Cell **18**, 1213–1225.
Liu C, Moschou PN. 2018. Phenotypic novelty by CRISPR in plants. Developmental Biology **435**, 170–175.
Liu H, Nonomura K-I. 2016. A wide reprogramming of histone H3 modifications during male meiosis I in rice is dependent on the Argonaute protein MEL1. Journal of Cell Science **129**, 3553–3561.
Liu M, Shi S, Zhang S, Xu P, Lai J, Liu Y, Yuan D, Wang Y, Du J, Yang C. 2014. SUMO E3 ligase AtMMS21 is required for normal meiosis and gametophyte development in Arabidopsis. BMC Plant Biol **14**, 153.
Liu J, Tang X, Gao L, *et al.* 2012. A role of tomato UV-Damaged DNA Binding Protein 1 (DDB1) in organ size control via an epigenetic manner. PLOS ONE **7**, e42621.
Liu C, Wu D, Wang L, Dang J, He Q, Guo Q, Liang G. 2018. Cis-regulated additively expressed genes play a fundamental role in the formation of triploid loquat (Eriobotrya japonica (Thunb.) Lindl.) heterosis. Molecular Genetics and Genomics **293**, 967–981.
Long JC, Xia AA, Liu JH, Jing JL, Wang YZ, Qi CY, He Y. 2018. Decrease in DNA methylation 1 (DDM1) is required for the formation of mCHH islands in maize. Journal of Integrative Plant Biology **61**, 749–764.
Lorković ZJ, Park C, Goiser M, Jiang D, Kurzbauer M-T, Schlögelhofer P, Berger F. 2017. Compartmentalization of DNA damage response between heterochromatin and euchromatin is mediated by distinct H2A histone variants. Current Biology **27**, 1192–1199.
Maher B. 2008. Personal genomes: The case of the missing heritability. Nature **456**, 18–21.
Maheshwari S, Tan EH, West A, Franklin FCH, Comai L, Chan SWL. 2015. Naturally occurring differences in CENH3 affect chromosome segregation in zygotic mitosis of hybrids. PLOS Genetics **11**, e1004970.
Manning K, Tor M, Poole M, Hong Y, Thompson AJ, King GJ, Giovannoni JJ, Seymour GB. 2006. A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. Nature Genetics **38**, 948–952.
Marand AP, Jansky SH, Zhao H, *et al.* 2017. Meiotic crossovers are associated with open chromatin and enriched with Stowaway transposons in potato. Genome Biology **18**, 203.

Marfil CF, Asurmendi S, Masuelli RW. 2012. Changes in micro RNA expression in a wild tuber-bearing Solanum species induced by 5-Azacytidine treatment. Plant Cell Reports **31**, 1449–1461.
Martinez-Garcia M, Schubert V, Osman K, Darbyshire A, Sanchez-Moran E, Franklin FCH. 2018. TOPII and chromosome movement help remove interlocks between entangled chromosomes during meiosis. Journal of Cell Biology **217**, 4070–4079.
Martínez G, Panda K, Köhler C, Slotkin RK. 2016. Silencing in sperm cells is directed by RNA movement from the surrounding nurse cell. Nature Plants **2**, 16030.
Martinez G, Wolff P, Wang Z, Moreno-Romero J, Santos-González J, Conze LL, DeFraia C, Slotkin RK, Köhler C. 2018. Paternal easiRNAs regulate parental genome dosage in Arabidopsis. Nature Genetics **50**, 193–198.
Mascher M, Gundlach H, Himmelbach A, *et al.* 2017. A chromosome conformation capture ordered sequence of the barley genome. Nature **544**, 427.
Mathieu O, Jasencakova Z, Vaillant I, Gendrel A-V, Colot V, Schubert I, Tourmente S. 2003. Changes in 5S rDNA chromatin organization and transcription during heterochromatin establishment in Arabidopsis. Plant Cell **15**, 2929–2939.
Matsumoto M, Matsutani S, Sugita K, *et al.* 1992. Depudecin: a novel compound inducing the flat phenotype of NIH3T3 cells doubly transformed by ras- and src-oncogene, produced by Alternaria brassicicola. Journal of Antibiotics **45**, 879–885.
Matzke MA, Mosher RA. 2014. RNA-directed DNA methylation: an epigenetic pathway of increasing complexity. Nature Reviews Genetics **15**, 394–408.
McGinty RK, Tan S. 2015. Nucleosome structure and function. Chem Rev **115**, 2255–2273.
Mehta GD, Rizvi SMA, Ghosh SK. 2012. Cohesin: A guardian of genome integrity. Biochimica et Biophysica Acta (BBA) - Molecular Cell Research **1823**, 1324–1342.
Mérai Z, Chumak N, García-Aguilar M, *et al.* 2014. The AAA-ATPase molecular chaperone Cdc48/p97 disassembles sumoylated centromeres, decondenses heterochromatin, and activates ribosomal RNA genes. Proceedings of the National Academy of Sciences of the United States of America **111**, 16166–16171.
Mercier R, Vezon D, Bullier E, Motamayor JC, Sellier A, Lefèvre F, Pelletier G, Horlow C. 2001. SWITCH1 (SWI1): a novel protein required for the establishment of sister chromatid cohesion and for bivalent formation at meiosis. Genes & Development **15**, 1859–1871.
Mittelsten Scheid O, Afsar K, Paszkowski J. 2003. Formation of stable epialleles and their paramutation-like interaction in tetraploid Arabidopsis thaliana. Nature Genetics **34**, 450.
Moore JW, Loake GJ, Spoel SH. 2011. Transcription dynamics in plant immunity. Plant Cell **23**, 2809–2820.
Mosher RA, Melnyk CW, Kelly KA, Dunn RM, Studholme DJ, Baulcombe DC. 2009. Uniparental expression of PolIV-dependent siRNAs in developing endosperm of Arabidopsis. Nature **460**, 283–286.
Nasmyth K. 2001. Disseminating the genome: Joining, resolving, and separating sister chromatids during mitosis and meiosis. Annual Review of Genetics **35**, 673–745.
Nasuda S, Hudakova S, Schubert I, Houben A, Endo TR. 2005. Stable barley chromosomes without centromeric repeats. Proceedings of the National Academy of Sciences of the United States of America **102**, 9842–9847.
Okada T, Endo M, Singh MB, Bhalla PL. 2005. Analysis of the histone H3 gene family in Arabidopsis and identification of the male-gamete-specific variant AtMGH3. Plant Journal **44**, 557–568.
Oliver SN, Finnegan EJ, Dennis ES, Peacock WJ, Trevaskis B. 2009. Vernalization-induced

flowering in cereals is associated with changes in histone methylation at the VERNALIZATION1 gene. Proceedings of the National Academy of Sciences of the United States of America **106**, 8386–8391.
Oliver C, Pradillo M, Corredor E, Cuñado N. 2013. The dynamics of histone H3 modifications is species-specific in plant meiosis. Planta **238**, 23–33.
Olmedo-Monfil V, Durán-Figueroa N, Arteaga-Vázquez M, Demesa-Arévalo E, Autran D, Grimanelli D, Slotkin RK, Martienssen RA, Vielle-Calzada JP. 2010. Control of female gamete formation by a small RNA pathway in Arabidopsis. Nature **464**, 628–632.
Ong-Abdullah M, Ordway JM, Jiang N, *et al.* 2015. Loss of Karma transposon methylation underlies the mantled somaclonal variant of oil palm. Nature **525**, 533–537.
Ono T, Fang Y, Spector DL, Hirano T. 2004. Spatial and temporal regulation of Condensins I and II in mitotic chromosome assembly in human cells. Molecular Biology of the Cell **15**, 3296–3308.
Palmgren MG, Edenbrandt AK, Vedel SE, *et al.* 2015. Are we ready for back-to-nature crop breeding? Trends in Plant Science **20**, 155–164.
Pandey P, Houben A, Kumlehn J, Melzer M, Rutten T. 2013. Chromatin alterations during pollen development in Hordeum vulgare. Cytogenetic and Genome Research **141**, 50–57.
Pecinka A, Abdelsamad A, Vu GTH. 2013. Hidden genetic nature of epigenetic natural variation in plants. Trends in Plant Sciencei **18**, 625–632.
Pecinka A, Dinh HQ, Baubec T, Rosa M, Lettner N, Scheid OM. 2010. Epigenetic regulation of repetitive elements is attenuated by prolonged heat stress in Arabidopsis. Plant Cell **22**, 3118–3129.
Pecinka A, Liu C-H. 2014. Drugs for plant chromosome and chromatin research. Cytogenetic and Genome Research **143**, 51–59.
Pecinka A, Mittelsten Scheid O. 2012. Stress-induced chromatin changes: a critical view on their heritability. Plant & Cell Physiology **53**, 801–808.
Pecinka A, Schubert V, Meister A, Kreth G, Klatte M, Lysak M, Fuchs J, Schubert I. 2004. Chromosome territory arrangement and homologous pairing in nuclei of Arabidopsis thaliana are predominantly random except for NOR-bearing chromosomes. Chromosoma **113**, 258–269.
Périlleux C, Pieltain A, Jacquemin G, *et al.* 2013. A root chicory MADS box sequence and the Arabidopsis flowering repressor FLC share common features that suggest conserved function in vernalization and de-vernalization responses. Plant Journal **75**, 390–402.
Phillips D, Nibau C, Wnetrzak J, Jenkins G. 2012. High Resolution Analysis of Meiotic Chromosome Structure and Behaviour in Barley (Hordeum vulgare L.). PLoS One **7**.
Pietzenuk B, Markus C, Gaubert H, Bagwan N, Merotto A, Bucher E, Pecinka A. 2016. Recurrent evolution of heat-responsiveness in Brassicaceae COPIA elements. Genome Biology **17**, 209.
Pignatta D, Novitzky K, Satyaki PR V, Gehring M. 2018. A variably imprinted epiallele impacts seed development. PLoS Genetics **14**, e1007469.
Pillot M, Baroux C, Vazquez MA, Autran D, Leblanc O, Vielle-Calzada JP, Grossniklaus U, Grimanelli D. 2010. Embryo and endosperm inherit distinct chromatin and transcriptional states from the female gametes in Arabidopsis. Plant Cell **22**, 307–320.
Porto DD, Bruneau M, Perini P, Anzanello R, Renou J-P, Santos HP dos, Fialho FB, Revers LF. 2015. Transcription profiling of the chilling requirement for bud break in apples: a putative role for FLC-like genes. Journal of Experimental Botany **66**, 2659–2672.
Pradillo M, Knoll A, Oliver C, Varas J, Corredor E, Puchta H, Santos JL. 2015. Involvement of

the cohesin cofactor PDS5 (SPO76) during meiosis and DNA repair in Arabidopsis thaliana. Frontiers in Plant Science **6**, 1034.
Prusicki MA, Keizer EM, van Rosmalen RP, Komaki S, Seifert F, Müller K, Wijnker E, Fleck C, Schnittger A. 2019. Live cell imaging of meiosis in Arabidopsis thaliana. eLife **8**, e42834.
Quadrana L, Colot V. 2016. Plant transgenerational epigenetics. Annual Reviews in Genetics **50**, 467–491.
Raja P, Sanville BC, Buchmann RC, Bisaro DM. 2008. Viral genome methylation as an epigenetic defense against geminiviruses. Journal of Virology **82**, 8997–9007.
Rakyan VK, Down TA, Balding DJ, Beck S. 2011. Epigenome-wide association studies for common human diseases. Nature Reviews Genetics **12**, 529.
Ramírez-González RH, Borrill P, Lang D, *et al.* 2018. The transcriptional landscape of polyploid wheat. Science **361**, eaar6089.
Ramirez-Prado JS, Piquerez SJM, Bendahmane A, Hirt H, Raynaud C, Benhamed M. 2018. Modify the histone to win the battle: Chromatin dynamics in plant-pathogen interactions. Frontiers in Plant Science **9**, 355.
Ravi M, Chan SWL. 2010. Haploid plants produced by centromere-mediated genome elimination. Nature **464**, 615–618.
Reeves PH, Ellis CM, Ploense SE, *et al.* 2012. A regulatory network for coordinated flower maturation. PLOS Genetics **8**, e1002506.
Richards DM, Greer E, Martin AC, Moore G, Shaw PJ, Howard M. 2012. Quantitative dynamics of telomere bouquet formation. PLoS Computational Biology **8**, e1002812–e1002812.
Roberts NY, Osman K, Armstrong SJ. 2009. Telomere distribution and dynamics in somatic and meiotic nuclei of Arabidopsis thaliana. Cytogenetic and Genome Research **124**, 193–201.
Rockmill B, Voelkel-Meiman K, Roeder GS. 2006. Centromere-proximal crossovers are associated with precocious separation of sister chromatids during meiosis in Saccharomyces cerevisiae. Genetics **174**, 1745–1754.
Roessler K, Bousios A, Meca E, Gaut BS. 2018. Modeling interactions between transposable elements and the plant epigenetic response: Reliance on element retention. Genome Biology and Evolution **10**, 803–815.
Rosa S, Shaw P. 2013. Insights into chromatin structure and dynamics in plants. Biology **2**, 1378–1410.
Roudier F, Ahmed I, Berard C, *et al.* 2011. Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. EMBO Journal **30**, 1928–1938.
Ruelens P, de Maagd RA, Proost S, Theißen G, Geuten K, Kaufmann K. 2013. FLOWERING LOCUS C in monocots and the tandem origin of angiosperm-specific MADS-box genes. Nature Communications **4**, 2280.
Russell SD, Gou X, Wong CE, Wang X, Yuan T, Wei X, Bhalla PL, Singh MB. 2012. Genomic profiling of rice sperm cell transcripts reveals conserved and distinct elements in the flowering plant male germ lineage. New Phytologist **195**, 560–573.
Rutowicz K, Puzio M, Halibart-Puzio J, *et al.* 2015. A specialized histone H1 variant is required for adaptive responses to complex abiotic stress and related DNA methylation in Arabidopsis. Plant Physiology **169**, 2080–2101.
Sandhu D, Gill KS. 2002. Gene-containing regions of wheat and the other grass genomes. Plant Physiology **128**, 803–811.
Sanei M, Pickering R, Kumke K, Nasuda S, Houben A. 2011. Loss of centromeric histone H3 (CENH3) from centromeres precedes uniparental chromosome elimination in interspecific

barley hybrids. Proceedings of the National Academy of Sciences of the United States of America **108**, E498–E505.
Schmiesing JA, Gregson HC, Zhou S, Yokomori K. 2000. A human condensin complex containing hCAP-C-hCAP-E and CNAP1, a homolog of Xenopus XCAP-D2, colocalizes with phosphorylated histone H3 during the early stage of mitotic chromosome condensation. Molecular and Cellular Biology **20**, 6996–7006.
Schmitz RJ, He Y, Valdes-Lopez O, *et al.* 2013*a*. Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. Genome Research **23**, 1663–1674.
Schmitz RJ, Schultz MD, Urich MA, *et al.* 2013*b*. Patterns of population epigenomic diversity. Nature **495**, 193–198.
Schoft VK, Chumak N, Mosiolek M, Slusarz L, Komnenovic V, Brownfield L, Twell D, Kakutani T, Tamaru H. 2009. Induction of RNA-directed DNA methylation upon decondensation of constitutive heterochromatin. EMBO Reports **10**, 1015–1021.
Schubert V, Klatte M, Pecinka A, Meister A, Jasencakova Z, Schubert I. 2006. Sister chromatids are often incompletely aligned in meristematic and endopolyploid interphase nuclei of Arabidopsis thaliana. Genetics **172**, 467–475.
Sequeira-Mendes J, Aragüez I, Peiró R, Mendez-Giraldez R, Zhang X, Jacobsen SE, Bastolla U, Gutierrez C. 2014. The functional topography of the Arabidopsis genome is organized in a reduced number of linear motifs of chromatin states. Plant Cell **26**, 2351–2366.
Shao T, Tang D, Wang KJ, Wang M, Che LX, Qin BX, Yu HX, Li M, Gu MH, Cheng ZK. 2011. OsREC8 is essential for chromatid cohesion and metaphase I monopolar orientation in rice meiosis. Plant Physiology **156**, 1386–1396.
She W, Grimanelli D, Rutowicz K, Whitehead MWJ, Puzio M, KotliŃ„ski M, Jerzmanowski A, Baroux C. 2010. Chromatin reprogramming during the somatic-to-reproductive cell fate transition in plants. Development **140**, 4008.
Sheehan MJ, Pawlowski WP. 2009. Live imaging of rapid chromosome movements in meiotic prophase I in maize. Proceedings of the National Academy of Sciences of the United States of America **106**, 20989–20994.
Shen X, Xu L, Liu Y, Dong H, Zhou D, Zhang Y, Lin S, Cao J, Huang L. 2019. Comparative transcriptome analysis and ChIP-sequencing reveals stage-specific gene expression and regulation profiles associated with pollen wall formation in Brassica rapa. BMC Genomics **20**, 264.
Shen Y, Zhang J, Liu Y, Liu S, Liu Z, Duan Z, Wang Z, Zhu B, Guo Y-L, Tian Z. 2018. DNA methylation footprints during soybean domestication and improvement. Genome Biology **19**, 128.
Shi J, Dong A, Shen W-H. 2015. Epigenetic regulation of rice flowering and reproduction. Frontiers in Plant Science **5**, 803.
Shroff R, Arbel-Eden A, Pilch D, Ira G, Bonner WM, Petrini JH, Haber JE, Lichten M. 2004. Distribution and dynamics of chromatin modification induced by a defined DNA double-strand break. Current Biology **14**, 1703–1711.
Sidhu GK, Fang C, Olson MA, Falque M, Martin OC, Pawlowski WP. 2015. Recombination patterns in maize reveal limits to crossover homeostasis. Proceedings of the National Academy of Sciences of the United States of America **112**, 15982–15987.
Slotkin RK, Vaughn M, Borges F, Tanurdžić M, Becker JD, Feijó JA, Martienssen RA. 2009. Epigenetic reprogramming and small RNA silencing of transposable elements in pollen. Cell **136**, 461–472.
Smith SJ, Osman K, Franklin FCH. 2014. The condensin complexes play distinct roles to

ensure normal chromosome morphogenesis during meiotic division in Arabidopsis. Plant Journal **80**, 255–268.
Song Q, Zhang T, Stelly DM, Chen ZJ. 2017. Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. Genome Biology **18**, 99.
Song T, Zhang Q, Wang H, Han J, Xu Z, Yan S, Zhu Z. 2018. OsJMJ a rice histone demethylase gene, plays key roles in plant development and responds to drought stress. Plant Physiology and Biochemistry **703**, 183–188.
Steward N, Ito M, Yamaguchi Y, Koizumi N, Sano H. 2002. Periodic DNA methylation in maize nucleosomes and demethylation by environmental stress. Journal of Biological Chemistry **277**, 37741–37746.
Stroud H, Otero S, Desvoyes B, Ramírez-Parra E, Jacobsen SE, Gutierrez C. 2012. Genome-wide analysis of histone H3.1 and H3.3 variants in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America **109**, 5370–5375.
Takuno S, Ran J-H, Gaut BS. 2016. Evolutionary patterns of genic DNA methylation vary across land plants. Nature Plants **2**, 15222.
Teyssier E, Bernacchia G, Maury S, How Kit A, Stammitti-Bert L, Rolin D, Gallusci P. 2008. Tissue dependent variations of DNA methylation and endoreduplication levels during tomato fruit development and ripening. Planta **228**, 391–399.
Thieme M, Lanciano S, Balzergue S, Daccord N, Mirouze M, Bucher E. 2017. Inhibition of RNA polymerase II allows controlled mobilisation of retrotransposons for plant breeding. Genome Biology **18**, 134.
Tian L, Fong MP, Wang JJ, Wei NE, Jiang H, Doerge RW, Chen ZJ. 2005. Reversible histone acetylation and deacetylation mediate genome-wide, promoter-dependent and locus-specific changes in gene expression during plant development. Genetics **169**, 337–345.
Tittel-Elmer M, Bucher E, Broger L, Mathieu O, Paszkowski J, Vaillant I. 2010. Stress-induced activation of heterochromatic transcription. PLoS Genetics **6**, e1001175.
Trujillo JT, Beilstein MA, Mosher RA, Seetharam AS, Hufford MB. 2018. Evidence for a Unique DNA-Dependent RNA Polymerase in Cereal Crops. Molecular Biology and Evolution **35**, 2454–2462.
Underwood CJ, Choi K, Lambing C, *et al.* 2018. Epigenetic activation of meiotic recombination near Arabidopsis thaliana centromeres via loss of H3K9me2 and non-CG DNA methylation. Genome Research **28**, 519–531.
Vanyushin BF, Alexandrushkina NI, Kirnos MD. 1988. N6-Methyladenine in mitochondrial DNA of higher plants. FEBS Letters **233**, 397–399.
Venetsky A, Levy-Zamir A, Khasdan V, Domb K, Kashkush K. 2015. Structure and extent of DNA methylation-based epigenetic variation in wild emmer wheat (T. turgidum ssp. dicoccoides) populations. BMC Plant Biology **15**, 200.
Verkest A, Byzova M, Martens C, *et al.* 2015. Selection for improved energy use efficiency and drought tolerance in canola results in distinct transcriptome and epigenome changes. Plant Physiology **168**, 1338–1350.
Vlot AC, Dempsey DA, Klessig DF. 2009. Salicylic Acid, a multifaceted hormone to combat disease. Annual Reviews in Phytopathology **47**, 177–206.
Wako T, Houben A, Furushima-Shimogawara R, Belyaev ND, Fukui K. 2003. Centromere-specific acetylation of histone H4 in barley detected through three-dimensional microscopy. Plant Molecular Biology **51**, 533–541.
Wako T, Murakami Y, Fukui K. 2005. Comprehensive analysis of dynamics of histone H4

acetylation in mitotic barley cells. Genes & Genetic Systems **80**, 269–276.
Walker J, Gao H, Zhang J, Aldridge B, Vickers M, Higgins JD, Feng X. 2018. Sexual-lineage-specific DNA methylation regulates meiosis in Arabidopsis. Nature Genetics **50**, 130–137.
Wang Z, Casas-Mollano JA, Xu J, Riethoven J-JM, Zhang C, Cerutti H. 2015*a*. Osmotic stress induces phosphorylation of histone H3 at threonine 3 in pericentromeric regions of Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America **112**, 8487–8492.
Wang C, Gao F, Wu J, Dai J, Wei C, Li Y. 2010. Arabidopsis putative deacetylase AtSRT2 regulates basal defense by suppressing PAD4, EDS5 and SID2 expression. Plant Cell Physiology **51**, 1291–1299.
Wang M, Tang D, Wang KJ, Shen Y, Qin BX, Miao CB, Li M, Cheng ZK. 2011. OsSGO1 maintains synaptonemal complex stabilization in addition to protecting centromeric cohesion during rice meiosis. Plant Journal **67**, 583–594.
Wang L-C, Wu J-R, Hsu Y-J, Wu S-J. 2015*b*. Arabidopsis HIT4, a regulator involved in heat-triggered reorganization of chromatin and release of transcriptional gene silencing, relocates from chromocenters to the nucleolus in response to heat stress. New Phytologist **205**, 544–554.
Waters AJ, Bilinski P, Eichten SR, Vaughn MW, Ross-Ibarra J, Gehring M, Springer NM. 2013. Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. Proceedings of the National Academy of Sciences of the United States of America **110**, 19639–19644.
Whittaker C, Dean C. 2017. The FLC locus: A platform for discoveries in epigenetics and adaptation. Annual Review of Cell and Developmental Biology **33**, 555–575.
Willing E-M, Piofczyk T, Albert A, Winkler BJ, Schneeberger K, Pecinka A. 2016. UVR2 ensures trans-generational genome stability under simulated natural UV-B in Arabidopsis thaliana. Nature Communications **7**, 13522.
Wollmann H, Holec S, Alden K, Clarke ND, Jacques P-É, Berger F. 2012. Dynamic Deposition of Histone Variant H3.3 Accompanies Developmental Remodeling of the Arabidopsis Transcriptome. PLOS Genetics **8**, e1002658.
Xianwei S, Zhang X, Sun J, Cao X. 2015. Epigenetic mutation of RAV6 affects leaf angle and seed size in rice. Plant Physiology **169**, 2118–2128.
Xie N, Zhou Y, Sun Q, Tang B. 2018. Novel epigenetic techniques provided by the CRISPR/Cas9 system. Stem Cells International **2018**, 1–12.
Xu J, Tanino KK, Robinson SJ. 2016. Stable epigenetic variants selected from an induced hypomethylated Fragaria vesca population. Frontiers in Plant Science **7**, 1–14.
Yang XH, Boateng KA, Strittmatter L, Burgess R, Makaroff CA. 2009. Arabidopsis Separase functions beyond the removal of sister chromatid cohesion during meiosis. Plant Physiology **151**, 323–333.
Yang C, Hamamura Y, Sofroni K, Böwer F, Stolze SC, Nakagami H, Schnittger A. 2019. SWITCH 1/DYAD is a WINGS APART-LIKE antagonist that maintains sister chromatid cohesion in meiosis. Nature Communications **10**, 1755.
Yang H, Liu X, Xin M, Du J, Hu Z, Peng H, Rossi V, Sun Q, Ni Z, Yao Y. 2016. Genome-wide mapping of targets of maize histone deacetylase HDA101 reveals its function and regulatory mechanism during seed development. Plant Cell **28**, 629–645.
Yang XH, Timofejeva L, Ma H, Makaroff CA. 2006. The Arabidopsis SKP1 homolog ASK1 controls meiotic chromosome remodeling and release of chromatin from the nuclear membrane and nucleolus. Journal of Cell Science **119**, 3754–3763.

Yelagandula R, Stroud H, Holec S, *et al.* 2014. The histone variant H2A.W defines heterochromatin and promotes chromatin condensation in Arabidopsis. Cell **158**, 98–109.
Yuan G, Ahootapeh BH, Komaki S, Schnittger A, Lillo C, De Storme N, Geelen D. 2018. PROTEIN PHOSHATASE 2A B'α and β maintain centromeric sister chromatid cohesion during meiosis in Arabidopsis. Plant Physiology **178**, 317–328.
Yuan J, Guo X, Hu J, Lv Z, Han F. 2014. Characterization of two CENH3 genes and their roles in wheat evolution. New Phytologist **206**, 839–851.
Yuan L, Yang XH, Makaroff CA. 2011. Plant cohesins, common themes and unique roles. Current Protein & Peptide Science **12**, 93–104.
Zamariola L, De Storme N, Vannerum K, Vandepoele K, Armstrong SJ, Franklin FCH, Geelen D. 2014. SHUGOSHINs and PATRONUS protect meiotic centromere cohesion in Arabidopsis thaliana. Plant Journal **77**, 782–794.
Zelkowski M, Zelkowska K, Conrad U, Hesse S, Lermontova I, Marzec M, Meister A, Houben A, Schubert V. 2019. Arabidopsis NSE4 proteins act in somatic nuclei and meiosis to ensure plant viability and fertility. Frontiers in Plant Science **10**, 774.
Zemach A, Kim MY, Hsieh P-H, Coleman-Derr D, Eshed-Williams L, Thao K, Harmer SL, Zilberman D. 2013. The Arabidopsis nucleosome remodeler DDM1 allows DNA methyltransferases to access H1-containing heterochromatin. Cell **153**, 193–205.
Zemach A, Kim MY, Silva P, Rodrigues JA, Dotson B, Brooks MD, Zilberman D. 2010. Local DNA hypomethylation activates genes in rice endosperm. Proceedings of the National Academy of Sciences of the United States of America **107**, 18729–18734.
Zhang X. 2012. Chromatin modifications in plants. In: Wendel FJ,, In: Greilhuber J,, In: Dolezel J,, In: Leitch JI, eds. Plant genome diversity Vol 1: Plant genomes, their residents, and their evolutionary dynamics. Vienna: Springer Vienna, 237–255.
Zhang L, Cheng Z, Qin R, *et al.* 2012. Identification and characterization of an epi-allele of FIE1 reveals a regulatory linkage between two epigenetic marks in rice. Plant Cell **24**, 4407–4421.
Zhang Y-Y, Latzel V, Fischer M, Bossdorf O. 2018*a*. Understanding the evolutionary potential of epigenetic variation: a comparison of heritable phenotypic variation in epiRILs, RILs, and natural ecotypes of Arabidopsis thaliana. Heredity **121**, 257–265.
Zhang XL, Li XX, Marshall JB, Zhong CX, Dawe RK. 2005. Phosphoserines on maize CENTROMERIC HISTONE H3 and histone H3 demarcate the centromere and pericentromere during chromosome segregation. Plant Cell **17**, 572–583.
Zhang Y-C, Liao J-Y, Li Z-Y, Yu Y, Zhang J-P, Li Q-F, Qu L-H, Shu W-S, Chen Y-Q. 2014. Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. Genome Biology **15**, 512.
Zhang Q, Wang D, Lang Z, *et al.* 2016. Methylation interactions in Arabidopsis hybrids require RNA-directed DNA methylation and are influenced by genetic variation. Proceedings of the National Academy of Sciences of the United States of America **113**, 4248–4256.
Zhang S, Wang D, Zhang H, Skaggs MI, Lloyd A, Ran D, An L, Schumaker KS, Drews GN, Yadegari R. 2018*b*. FERTILIZATION-INDEPENDENT SEED-Polycomb Repressive Complex 2 plays a dual role in regulating type I MADS-box genes in early endosperm development. Plant Physiology, 285–299.
Zhong S, Fei Z, Chen Y-R, *et al.* 2013. Single-base resolution methylomes of tomato fruit development reveal epigenome modifications associated with ripening. Nature Biotechnology **31**, 154–159.
Zhou A, Pawlowski WP. 2014. Regulation of meiotic gene expression in plants. Frontiers in

Plant Science **5**, 413.
Zhou C, Zhang L, Duan J, Miki B, Wu K. 2005. HISTONE DEACETYLASE19 is involved in jasmonic acid and ethylene signaling of pathogen response in Arabidopsis. Plant Cell **17**, 1196–1204.
Zhu J, Fang L, Yu J, Zhao Y, Chen F, Xia G. 2018. 5-Azacytidine treatment and TaPBF-D over-expression increases glutenin accumulation within the wheat grain by hypomethylating the Glu-1 promoters. Theoretical and Applied Genetics **131**, 735–746.
Zilberman D, Coleman-Derr D, Ballinger T, Henikoff S. 2008. Histone H2A.Z and DNA methylation are mutually antagonistic chromatin marks. Nature **456**, 125–129.

Figure legends

Fig. 1. Overview of stress-induced chromatin changes and their potential trajectories.
Environmentally-induced stresses lead to genome wide changes of transcript levels. These changes are accompanied by dynamic changes influencing chromatin compaction and also gene expression. Transcriptional and chromatin changes can be correlated or uncorrelated and the exact hierarchy of events determining these changes can vary accordingly to the plant species and type of stress. There are some evidences that both transcriptional and chromatin changes can persist after the removal of stress and can be mitotically inherited. In a transcriptional memory gene - high expression levels are persistent for a prolonged period of time even after the end of a stress cue. In case of recurring stress, the transcriptional response to a second stress cue is modified compared to the response the first exposure to the same stress. Many cases of memory also involve chromatin dynamics at key regulatory loci (epigenetic memory). Despite transcriptional and chromatin/epigenetic memory, resetting and recovery are likely the overriding strategies used by plants to maximize fitness in time and space.

Fig. 2. Overview of chromosome organisation during mitosis and meiosis.
At the onset of mitosis, chromatin condensation is necessary to disassemble the interphase chromatin in a process driven by specific post-translational modifications (PTMs) in H3 and condensin complexes. In addition, cohesin complex is essential for defining chromosome structure by providing a physical linkage between sister chromatids until their segregation at anaphase.
Throughout meiosis, condensin complexes I and II are required to maintain the structural integrity of chromosomes. During leptonema, the histone variant H2A.X is rapidly phosphorylated to γ-H2A.X at double-strand break (DSB) sites. The synaptonemal complex (SC) forms between paired chromosomes at zygonema, and full synapsis is reached at pachynema. TOPOISOMERASE II (TOPII) activity is essential for removal of the interlocks formed when homologous chromosomes trap other chromosomes in between them. During late prophase I (diplonema/diakinesis) the SC disappears and further condensing homologous chromosomes are held together by chiasmata. During anaphase I, loss of cohesion between the arms of sister chromatids allows the segregation of homologous chromosomes to the opposite poles. Centromeric cohesion is released at the onset of anaphase II and sister chromatids segregate to form a tetrad.

Fig. 3. Applications of epigenetic variation for the purposes of plant breeding.
Natural epigenetic variation is relatively little explored and known cases were often selected by the phenotype and only later described to have epigenetic basis. Presumably, genome-wide screening for natural epigenetic variation will allow less biased use of the naturally occurring germplasms in the future. In contrast, induced epigenetic variation is provoked by humans either in a targeted manner towards specific genomic locus or an untargeted manner

with subsequent identification and selection of the modified loci. Choice of the method(s) is guided by the purpose, the species and its available resources. Some of the artificially produced epialleles fall under the GMO regulations.

Figure 1

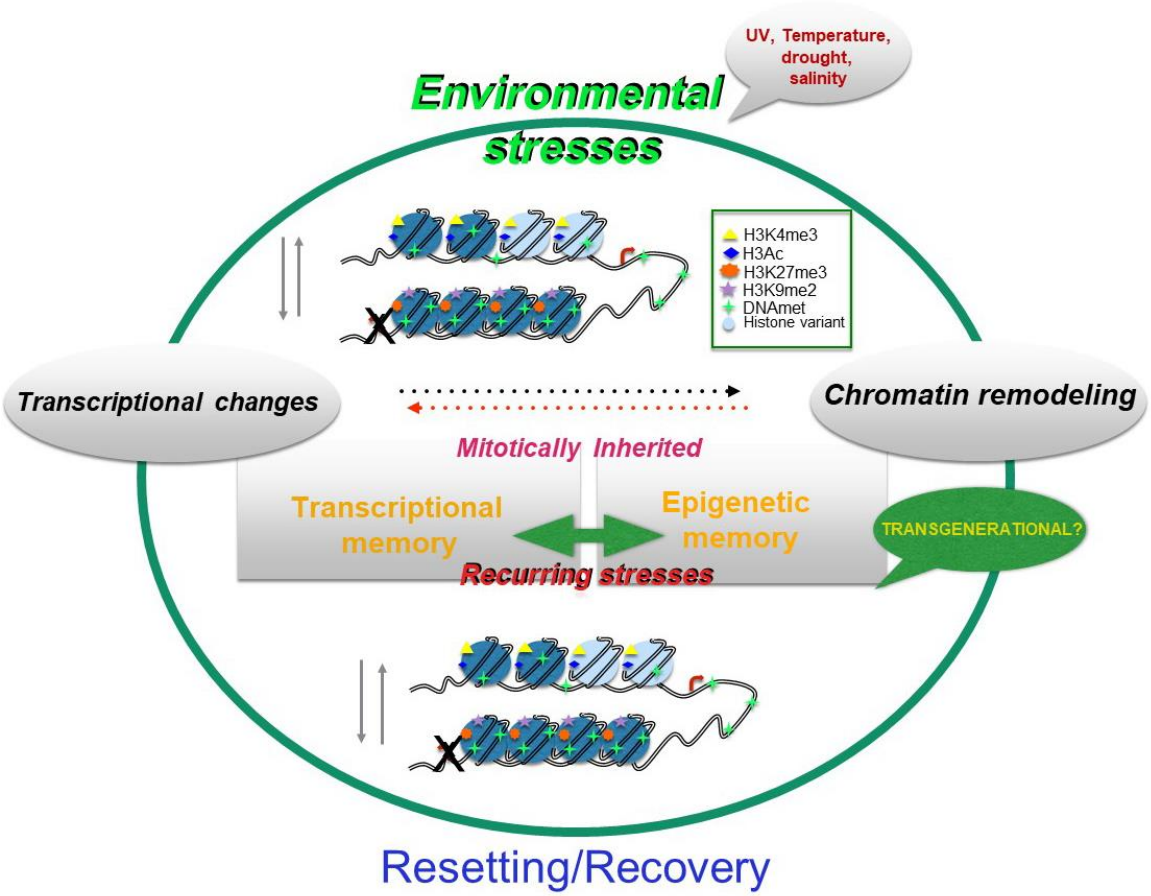

Figure 2

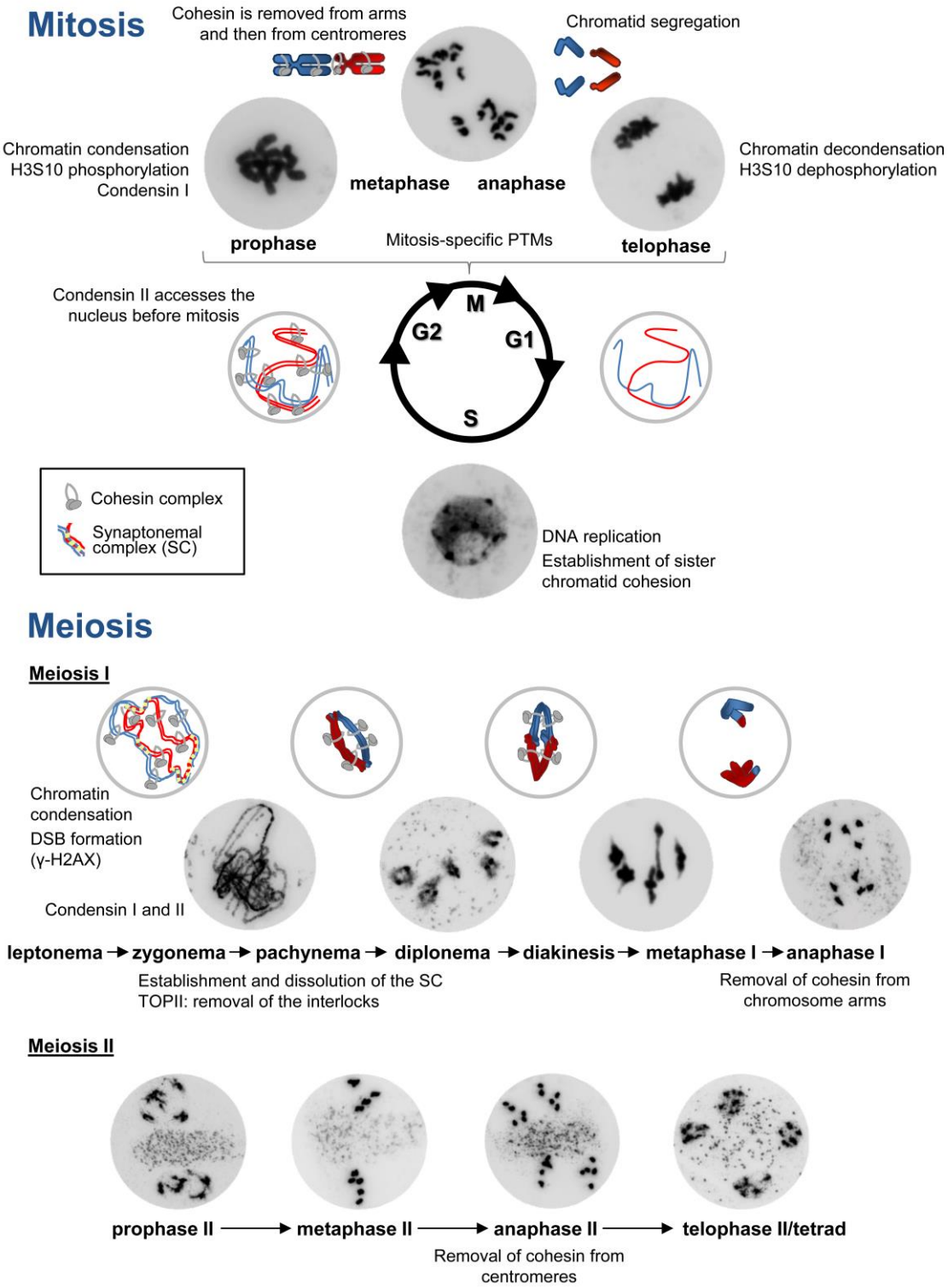

Figure 3